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Title: Perfect score:

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Sequence:

Scoring table:

Minimum DB : Maximum DB :

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DENEKALI INFORMATION:

SERVE Daniel

APPLICANT: Steve Daniel

APPLICANT: James Gilmore

APPLICANT: James Gilmore

APPLICANT: Susan G. Stuart

APPLICANT: Susan G. Stuart

APPLICANT: Susan G. Stuart

TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL

TITLE OF INVENTION: PROLIFERATION

TITLE OF INVENTION: PROLIFERATION

TITLE OF INVENTION: PROLIFERATION

CURRENT APPLICATION NUMBER: US/09/232,160

CURRENT APPLICATION NUMBER: US/09/232,160

CURRENT FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PERL PROGRAM

SOCTWARE: PERL PROGRAM

SEQ ID NO 13

LENGTH: 2029
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Mismatches:
Indels:
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US-09-907-794A-212
US-09-905-125A-212
US-09-902-775A-212
US-09-010-1478-19
US-08-340-4288-1
PCT-US93-07306-1
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US-09-103-429A-1
US-09-103-429A-2
US-08-225-477B-2
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                                                        US-09-023-655-876
US-09-566-921-97
US-08-242-097-1
US-08-242-097-1
US-09-206-695-1
US-09-799-118-1
US-09-484-970B-63
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PCT-US94-00253-2
US-08-225-477B-1
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09232160; Patent No. 6368794; GENERAL INFORMATION:
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US-09-232-160-13
TYPE: DNA
ORGANISM: Homo sapiens
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Query Match:
Percent Similarity:
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 Sequence 13, Appl
Sequence 200, App
Sequence 200, App
Sequence 200, App
Sequence 849, App
Sequence 853, App
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Sequence 12, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 15, Appl
Patent No. 5504194
                                                                                                                  4; Search time 97 Seconds
(without alignments)
1842.208 Million cell updates/sec
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-903-125A-200
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US-09-813-381-853
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US-09-724-864-28
US-08-892-880-12
US-08-892-880-13
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                                                                                       nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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## APPLICANT: Tunnas, Dannel
## APPLICANT: Williams, Paricey
## APPLICANT: World williams, Paricey
## APPLICANT: World williams, Paricey
## TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
## TITLE OF INVENTION: Acids Encoding the Same
## CURRENT FILMSO DATE: 10466-11-10
## PRIOR PELING DATE: 1046-11-10
## PRIOR PELING DATE: 1050-02-2
## PRIOR APPLICANTON NUMBER: US 60/143,048
## PRIOR APPLICANTON NUMBER: US 60/145,698
## PRIOR APPLICANTON NUMBER: US 60/145,698
## PRIOR APPLICANTON NUMBER: US 60/146,222
## PRIOR APPLICANTON NUMBER: US 60/146,222
## PRIOR APPLICANTON NUMBER: PCT/US99/2054
## PRIOR APPLICANTON NUMBER: PCT/US99/2051
## PRIOR PLING DATE: 1999-01-15
## PRIOR PLING DATE: 1999-10-05
## PRIOR APPLICANTON NUMBER: PCT/US99/3099
## PRIOR APPLICANTON NUMBER: PCT/US99/30999
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Matches:
Conservative:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                            Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                     Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                       Gerber, Hanspeter
Gerritsen, Mary E
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                       Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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ORGANISM: HOMO
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183 ATGGCCAGGTGCTTCAGCCTGGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 242
                                                                              363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422
                                                                                                                                                                                                                                                                                                                SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  903 CTAGTGCTTGCTCTCCTCTTTGGTGCTGCTGGTCTTGGATTTTGCTATGTCAA 962
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                                                                                                                                  41 ileThrieuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
                                                                                                                                                                                                                            CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
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                                                                                                                                                                                                                                                                                                                                                SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
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Patent No. 635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1143 GAAGTT 1148
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Ferrara, Napoleone
Filvaroff, Ellen
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Gerber, Hanspeter
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       RESULT 3
US-09-905-125A-200
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                                                   US-10-079-111-1 (1-322) x US-09-907-794A-200 (1-2372)
Mismatches:
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Transmembrane Polypeptides and Nucleic APPLICANT: MAILIANIS, TOTAL APPLICANT: MAILIANIS, MOOD, William, TITLE OF INVENTION: Secreted and Transmembrane FITTLE OF INVENTION: Acids Encoding the Same FILE SPERKENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-15
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PRIOR PRILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PRILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28256
PRIOR APPLICATION NUMBER: PCT/US99/28265
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-20
PRIOR PRILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: Sequence 200, Application US/09905125A
; Sequence 200, Application US/09905125A
; GENERAL INPORMATION:
 APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
 APPLICANT: Beatein, David
; APPLICANT: Eaton, Dan L. Gerritsen, Mary E.
Goddard, A.
Goddwski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, Williams, I.

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and Transmembrane Polypeptides and Nucleic
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APPLICANT: Hillan, Kenneth, J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Baon, Micholas F.
APPLICANT: Baon, Micholas F.
APPLICANT: Roy, Margatet Ann
APPLICANT: Roy, Margatet Ann
APPLICANT: Roy, Margatet Ann
APPLICANT: Millans, P. Mickey
APPLICANT: Willians, P. Mickey
APPLICANT: Willians, P. Mickey
APPLICANT: Willians, P. Mickey
APPLICANT: Millians, P. Mickey
APPLICANT: Millians, P. Mickey
APPLICANT: Millians, P. Mickey
APPLICANT: Modd, Willian, I.
TITLE OF INVENTION: Secreted and Transmembrane
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21091
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerritsen, Mary E. Goddard, A. Godowski, Paul J. Grimaldi, Christopher J Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P. Pani, James
                                                                                                                                                                                                                                                                                                                                                                                                      Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
                                                                                                                                                                                                                                                                                            APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Iuc
APPLICANT: Eaton, Dan L.
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Mismatches:
Indels:
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                                                                                                                               Matches:
                                                                                                 5.92e-177
1657.00
100.00%
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-125A-200
                                                                                                                                        Percent Similarity:
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Query Match:
                                                                                  Alignment Scores:
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Matches:
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION WUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR PPLING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
PRIOR FILING DATE: 2000-01-05
NUMBER OF SQ ID NOS: 423
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LENGTH: 2372
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; Sequence 849, Application US/0983381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TILLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs
; TILLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs
; TILLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT PILING DATE: 2001-04-11
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 849
; LENGTH: 2404
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                                                                                   AsplysasnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
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                                     GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
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Fatent No. 6672186
Fatent No. 6672186
FATEN INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
FRIOR APPLICATION NUMBER: 09/516,448
FRIOR APPLICATION NUMBER: 09/516,448
FRIOR FILING DATE: 2000-02-04-11
FRIOR FILING DATE: 2000-02-05
SOFTWARE: FEE TO NOS: 2050
SOFTWARE: FEES FOR Windows Version 3.0
SOFTWARE: PastSEQ for Windows Version 3.0
ELENTH: 2404
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CORGANISM: Homo sapiens
US-09-833-381-853
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Best Local Similarity:
Query Match:
DB:
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US-09-833-381-853
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Pred. No.:
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IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
                           ValGinGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
                                                                            CysArgLeuLeuGlyLeuSerLeuAlaGlyLygsAspGlnValGluThrAlaLeuLysAla
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Patent No. 5942417
GENERAL INFORMATION:
APPLICANT: NI, JIAN
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ORGANISM: Mouse
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US-09-724-864-28
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-UL-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFPE, ERIC K
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
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Matches:
                                                        ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & STREET: 1100 NEW YORK AVENUE, NW, SUITE CITY: WASHINGTON STATE: DC
                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 1488.0490001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
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                                                                                                                   ZIP: 20005-3934.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/09724864

| Sequence 28, Application US/09724864
| Patent NO. 6380362
| GENERAL INFORMATION:
| APPLICANT: Watson, James D
| APPLICANT: Watson, James G
| TITLE OF INVENTION: Polynuclectides and methods for their use:
| TITLE OF INVENTION: Dy the polynuclectides and methods for their use:
| TITLE OF INVENTION: Dy the polynuclectides and methods for their use:
| TITLE OF INVENTION: Dy The polynuclectides and methods for their use:
| TITLE OF INVENTION: Dy 1050U1
| CURRENT APPLICATION NUMBER: US/09/724,864
| CURRENT PLING DATE: 1999-12-23
| NUMBER OF SEQ ID NOS: 72
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 28
| LENGTH: 1896
                                                                        120
                                                                                                             450
                                                                                                                                                                                                                                                                                                                                 630
                                                                                                                                                                                                                                                                                                                                                                                                        069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
                                                                                                                                               SerArgGInPheAlaAlaTyrCysTyrAsnSerAspThrTrpThrAsnSerCysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
                                                                                               CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACAACAACA
                                                                                                                                                                                                                                                                                             GlubheileValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
                                                                                                                                                                                                                                                                                                                     ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                          CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                                                                      SerProhsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal
                                                                                                                                                                      ProGlu11e11eThrThrLysAspPro11ePheAsnThrGlnThrAlaThrGlnThrThr
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1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerlleTrpThrArgLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 ValGlnGlySerLeuArgAlaGluGluLeuSerlleGlnValSerCysArg1leMetGly
                               1015
        P.L.L.C.
                                                                                                                                                                                                                                                                                                               MEDIUM TIEE: LALUPLY LALUP
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATPORNEY/AGENT INFORMATION:
NAME: STEFFE, BRIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0490001
TELEPHONE: 202-371-2600
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83
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112
16
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                      APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER L.
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-079-111-1 (1-322) x US-08-892-880-12 (1-492)
                                                                                Sequence 12, Application US/08892880 Patent No. 5942417 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 base pairs
                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 492 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354.00
77.39%
72.17%
21.36%
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Best Local Similarity:
                                                               US-08-892-880-12
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                  SerTyrGlyTrpValGlyAspGlyPheValValileSerArglleSerProAsnProLys 105
                                                                                                                                                                                                                                                                                                   :::
194 AGAAACAAAAACCCACAGATGAATTTCACAGAAGCCAACGAGGGCCTGTAAGATGCTGGGA 253
                                                                                                                                                                                                                                                                                                                                                          CysGlyLysAsnGlyValGlyValLeuileTrpLysValProValSerArgGlnPheAla 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 ThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThrGluPhelleValger 165
                                                                                                                                                                                                                           26 ArgAlaGluGluLeuSerileGlnValSerCygArgileMetGlyIleThrLeuValSer 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlulysAlaAsnAspSerAsnProAsnGluGluSerLysLysThrAspLysAsnProGlu 305
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                                                                                                                                                                      SerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeuValGlnGlySerLeu
                                                                                                                                                                                                                                                                               46 LysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAlaCysArgLeuLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 AlaryrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIleProGlulletleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 ProAlaProAlaSerThrSerIleProArgArgLysLysLeulleCysValThrCluVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 GluSerLysSerProSerLysThrThrValArgCysLeuGluAlaGluVal 322
                                              1896
221
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62
4
                                                                        Conservative:
Mismatches:
                                                                                                                                        US-10-079-111-1 (1-322) x US-09-724-864-28 (1-1896)
                                              Length:
Matches:
                                                                                                      Indels:
                                            .62e-114
                                                        1103.00
79.18%
69.72%
66.57%
                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                          Alignment Scores:
US-09-724-864-28
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                                                                                                                                                                      255 CAAAGGAAAACTGNTTAAAAACCCAGTAGNAGTTCCAAGAGGTNCCAAGCAAAACTTACCG 314
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                                                          278 legluThrLysValVal-LysGluGluLysAlaAsnAspSerAsnPro-AsnGluGluSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 NEW YORK AVENUE, NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTHARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HERBHYTH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 1-5-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, BRIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0490001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: NI, JIAN
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN
                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08892880 Patent No. 5942417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.35e-23
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90.00%
88.57%
17.29%
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                       315 al-ArgCysteu 318
                                                                                                                                                                                                                                                           315 rercearecere 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: CDNA US-08-892-880-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: WASHINGTON STATE: DC
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                   RESULT 11
US-08-892-880-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 PheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThr 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 AlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyr 258
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                                                                                                                                                                                                                                                                                                                                                                                                 3: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 NEW YORK AVENUE, NW, SUITE 600
                                                                                                          --AspGlyPheValValIleSerArgIleSerPro
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89
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CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
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Matches:
                                  SerPheGluThrCysSerTyrGlyTrpValGly-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNAEL TOWN THE CANAL TOWN TELECOMMUNICATION IN PROPRATION:

TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           Sequence 13, Application US/08892880 Patent No. 5942417
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349.00
83.33%
82.41%
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TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE:
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STREET: 11
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Db   554 ATAACTATTGATAACCGCCACCGGTATGTCAAGAAAGGGGAATACGAACGA	THEI
OY 274 GILLysGluMetTleGluThrLysValValLysGluGluLysAlasnAsp-SerAshF 293 Db 74 CAGAGGGAATCATCAAAGGGAAGCGCAATCAACCCATGAATAGCAACCC 133 OY 293 CASAGGAATCAATCAACCAAACTAGTAAAGGGAAGCCCAATGAATAGCAACCC 133 Db 134 TAATGAGGAATCAAAACTGATAAAACCCAGTAAGGTCCAAGGCAAA 193 OY 313 TAATGAGGAATCAAAAACTGATAAAACCCAGTAAGGTCCAAGGCAAA 193 RESULT 12 \$504194  PAPLICATTON THILL OF VINEWATION: LYMPHOCYTE ADHESION RECEPTOR FOR HIGH  "RESULT 12 SGALBAN "RESULT 13 SGALBAN "RESULT 13 SGALBAN "RESULT 1	uValGlnGly 'CGTGCAGCTG 'CGTGCAGCTG TATATACCAC aCysArgleu

AsnProGlu 305

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GENERAL INFORMATION:
APPLICANT: HERRLICH, Peter
APPLICANT: PONTA, Helmut
APPLICANT: GURNTHERT, Ureula
APPLICANT: MATZKU, Siegfried
APPLICANT: MENZL, Achim
TITLE OF INVENTION: VALARANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
                                                                                                                                                                                                                                                                                                                                                   968 CATGAGTATCAGGATGAAGAG----GÁGACCCCACATGCTACAAGCACAACCTGGGCAGAT 1024
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                                                                                                                                                                                                                                                                                                              271 LysAsnGlnGlnLysGluMet1leGluThrLysValValLysGluGluLysAlaAsnAsp 290
                                                                                                                                                                                                                                   253 GlyLeuGlyPheCysTyrValLysArgTyrValLys-----AlaPheProPheThrAsn 270
                                                                                                                                                                                                                                                             908 AACAGCACCAGTGCTCATGGASAAACTGGACCCAGGAACCACAGCTCCTTTCAATAAC 967
LysLysLeulleCysValThrGluValPheMetGluThrSerThrMetSerThr---Glu 215
                                                                                                                                                        236 Val------ProThrAlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAla 252
                                                                                                     :::
848 ATCCATTCAAACCCAGAAGTACTACTTCAGACGACCACCAGGATGACTGATATAGACAGA
                          ThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #1.25
                                                                                                                                                                                                                                                                                                                                                                                              291 SerAsnProAsnGluGluSerLysLysThrAspLys---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,322
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,497
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7695,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08483322 Patent No. 5760178
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REFERENCE/DOCKET NUMBER: 165
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  548 CCAGTTACCATAACTATTGTCAACCGTGATGGCACCCGCTACAGCAGAAGAGGGCGAGTAT 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgileMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 96
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
        REGISTRATION NUMBER: 29,768
REFRENCE/DOCKET NUMBER: 16915/145
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5399
TELERAX: (202) 672-5399
TELERAX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3207 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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37.68%
25.22%
13.52%
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                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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DB:
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APPLICANT: PONTA, Helmut
APPLICANT: GUENTHERT, Ursula
APPLICANT: MATZKU, Siegfried
APPLICANT: WENZL, Achim
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
NUMBER OF SEQUENCES: 8
ADDRESSE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                     908 AACAGCACCAGTGCTCATGGAGAAAACTGGACCCAGGAACCACAGGCTCCTTTCAATAAC 967
                                                                                                                                                      291 SerAsnProAsnGluGluSerLysLysThrAspLys------AsnProGlu 305
                                --AlaPheProPheThrAsn 270
                                                                                                                      968 CATGAGTATCAGGATGAAGAG---GAGACCCCACATGCTACAAGCACAACCTGGGCAGAT
                                                                                        271 LysAsnGlnGlnLysGluMetIleGluThrLysValValLysGluGluLysAlaAsnAsp
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87
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,882
                           253 GlyLeuGlyPheCysTyrValLysArgTyrValLys--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 16915/145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/07/946,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08478882
Patent No. 5885575
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TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                         1085 CAGGGGAAGAACCCA 1099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3207 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Pred. No.:
Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ACATCACAGACCTACCCAATTCCTTCGATGGA 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 ThrGlnThrThrGluPheIleValSerAspSerThr---TyrSerValAlaSerProTyr 175
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                                                                                                                                                                                                                                                                                               ----SerlleTrpThr 16
                                                                                                                                                                                                                                                                                                                                                                                                                        37 ArglleMetGlyIleThrLeuValSerLysLaAsanGlnGlnLeuAsnPheThrGlu 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 -------ThrThrProProAla---ProAlaSerThrSerIleProArgArg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 LysLysLeulleCysValThrGluValPheMetGluThrSerThrMetSerThr---Glu 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       668 ICCACCAITGAGAAGAACACCCCAGAAGGCIACAITIIGCACACCGACCTICCCACIICA 727
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848 AICCAITCAAACCACAGAAGIACIACTICAGACAACCACCAGGAIGACIGAIAIAGACAGA 907
                                                                                                                                                                                                                                                                                                                                                         ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal
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Matches:
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දු පු	3	ArgCysPhe	ArgCysPheSerLeuValLeuLeuLeuThr      AgATCCTTTGGTTTCATCCTGCACATGA	1LeuThr ::: ?ATCATGGACAAGGTTT	ArgCysPheSerLeuValLeuLeuLeuThr	16 145
δy	17	ThrArgLeu	LeuValGlnGlySer	ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerlleGlnValS	erCys	36
Db	146	CTACTTTGC	cerceracagergage	ccreecacaccac	-U	205
ko i		ArgileMet	tGlyIleThrLeuVa.	SerLysLysAlaAsn( 	ArgileMetGlylleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	56 265
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or da	266	GCAGCTGAC	MAIACY SALGEGEE : CCTCTGCGAGGCTTT	CAACACCACCTTGCCC	GAGTTA	325
οχ	77	AlaLeuLys	sAlaSerPheGluTh: :	aLeulysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheV		9
Dp	326	GCCCTGAG	aaaggggtttgaaac	atgcaggtatgggttci	GGTA	382
Qy	97	IleSerArg	gIleSerProAsnPr	oLysCysGlyLysAsn(		а -
qq	383	ATCCCGAG	GATCCACCCCAACGC	TATCTGTGCAGCCAAC	ATCCCGAGGATCCACCCCAACGCTATCTGTGCAGCCAACAACACAGGAGTGTATATUCTC 	dr (
Qy	117	LysValPro	ovalSerArgGlnPh	eAlaAlaTyrCysTyr.	LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr :::	136
Db	443	CTCGCATC	CAACACCTCCCACTA	rgacacararriderre	crogoriccaacarcrocactargacacaratatracricaargerorroraa	502
È	137		sileProGluileil 	eThrThrLysAspPro	AsnSerCyslleProGluIlelleThrThrLysAspProIlePheAsnThrGluThrAla	156
qq	503	GAAGACTGT	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-ACATCAGTCACAGAC	-ACATCAGTCACAGACCTACCCAATTCCTTCGATGGA	54 /
٥٨	157		ThrGlnThrThrGluPheIleValSerAspSerThr-	SerAspSerThr	-TyrserValAlaSerProTyr	175
Db	548		CATAACTATTGTCAA	ccgrahracaktecec	CCAGTTACCATAACTATTGTCAACCGTGATGGCACCCGCTACAGCAAGAAGGGCGAGTAT	607
ζŏ	176	SerThr	1	-IleProAlaProThr		182
DP	608		CCAAGAAGACATCGA	TGCCTCAAACATTATA	  agaacaccaagaagacatcgatgcctcaaacattatagatgaggatgtcagcagtgga	667
λ	183	† † 1 1 1 1	Thrank Thrank	oProAlaProAla	-ThrThrProProAlaProAlaSerThrSerIleProArgArg	196
qo	668		TGAGAAGAGCACCCC	 !AGAAGGCTACATTTTG	TCCACCATTGAGAAGAGGCCCCAGAAGGCTACATTTTGCACACCGACCTTCCCACTTCA	727
δλ	197		ulleCysValThrGl	LysLysLeulleCysValThrGluValPheMetGluThrSerThrMetSerThr-	SerThrMetSerThrGlu	215
qu	728		TGGAGACCGGGATGA	ceccitétitaties	CAGCCTACTGGAGACCGGGATGACGCCTTCTTTATTGGGAGCACCCTGGCCACCATTGCA	787
٥٧	216		oPheValGluAsnLy	rsAlaAlaPheLysAsn	ThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGly	235
QQ	788		ATGGGTTTCTGCCCA	ACACAAAACAGAACCAG	  actactccatgggtttctgcccacacaaacagaaccaggacccagtggaaccc	847
δ	236	>	1	-ProThrAlaLeuValLeuAlaLeuLeuPhePheGlyAl	ıLeuPhePheGlyAlaAlaAla	252
Db	848		  aaacccagaagtaci	  ACTTCAGACAACCACC	::: atccattcaaacccagaagtactacttcagacaaccaccaggatgactgatatagacaga	907
ò	253		GlyLeuGlyPheCysTyrValLysArgTyrValLys-	rsArgTyrValLys	AlaPheProPheThrAsn	270
qq	908		ccagtgctcatggagi	AAACTGGACCCAGGAA	AACAGCACCAGTGCTCATGGAGAAACTGGACCCAGGAACCACAGCCTCCTTTCAATAAC	1967
ò	271		InGlnLysGluMetI 	leGluThrLysValVa] 	LysAsnGlnGlnLysGluMetIleGluThrLysValValLysGluGluLysAlaAsnAsp	290
qq	968		catgagtatcaggatgaaga	GAGACCCCACATGCT	-gagaccecacatectacaagcacaacctgggcagat	10
δλ	291		SerAsnProAsnGluGluSerLysLysThrAspLys-	ysLysThrAspLys		305

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                - nucleic search, using frame_plus_p2n model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Description	Description	D AF127670	7 AX136227	BD123566	AK075443	AR204700 Sequer	BD222718	AR410761	AX092274	AX454446	AX490924	AX697609	BD075532	BD172392	BD172711	BD173030	BD173349	BD175383	AY358925 Homo	BC026231	AF118108 Homo	AY372937 Bos t	BC038653 Mus	BC038892 Mus	AJ311501	AX136529	BD123769	AC009532	AY304537 Sus sci	6 BD076146 5' EST	ACLSOLU4 RACCUS	02 AC129402 RATTUS DO PD077623 5'EST OF	El 3 Continuation (4	00 BD073800 5'EST c	92 AR36549	Σ	M33827 H	AX401912	A M61875 Rattus	4A M27129 Mouse	M30655 M	7 BC061327 S	531 BC061531 Rattus	
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Catarrhini, Hominidae, Homo.
           CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
                                    301 TGTAGGCTGCGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
                                                                  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArgile
                                                                                                                                                                                                           AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTTAGGATT
                                                                                                                          SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal
                                                                                                                                                SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCyslle
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Hayashi,K.
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Patent: EP 1067182-A 149 10-JAN-2001;
Helix Research Institute (JP)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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           Arlz/670 1285 bp mRNA linear PRI 13-OCT-2000
Homo sapiens hyaluronic acid receptor (HAR) mRNA, complete cds.
AF127670
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SKKANQQLNFTBAKEA_RLLGISLAGKDQVETALKASFETCSYGWVGDGFVVISRISP
NPKCGKNGQULIWKVPVSRQPAAZYCNSSDYMYNSCIPEITTTKDP_FENTOTATOTT
BFIVSDSTYSYASPYESTPSTIPPAPAZSTSIPRRKKLICVTEVFMETSTMSTETEP
FVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVKRYVKRPFFTNKNQQKE
MIETKVVKEEKANDSNFNEESKKTDKNPEESKSPSKTTVRCLEAEV"
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Winkelmann,J.C., Basu,S., Ozdemir,E. and Blough,R.I.

Direct Submistain

Submitted (11-FEB-1999) Hematology-Oncology, University of Cincinnati, 231 Bethesda Avenue, Cincinnati, Onio 45267-0508, USA S (Bases 1 to 1285)

Winkelmann,J.C., Basu,S., Ozdemir,E. and Blough,R.I.

Direct Submission

Submitted (12-OCT-1999) Hematology-Oncology, University of Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, USA Sequence update by submitter

On Oct 13, 2000 this sequence version replaced gi:5732667.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1. (bases 1 to 1285)
                                                                                                                                                               Winkelmann, J.C., Basu, S., Ozdemir, E. and Blough, R.I. HAR: a novel homolog of CD44 and putative hyaluronic encoded by a gene on human chromosome 11p15 Unpublished
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11p15"
/gene="HAR"
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/db_xref="GI:10800122"
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/note="CD44 homolog"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1755)
Ota.T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
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07-JUL-2000 JP 2000253173
TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU
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PN JP 202017376-A/75

PD 22-JAN-2000

PF 07-JUL-2000 JP 2000253173

PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYAS

PI KOJI HAYASHI

PC C12N15/09, CO7K14/47, CO7K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
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/mol type="genomic DNA"
/db xref="taxon:9606"
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nprcgrnqvyliwkypvsropaaysysippapassipprnkclevivtryfwetstp
FVGSTYVASPYSTIPPATTTPPAPASTSIPRRKLICVTEVFWHTSTRNTETEP
FVGNRAAFKNEAAGFGCVPTALLVLALLFFGAAAGLGFCYVRRYVKRPFTNKNQQKE
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'n	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPhrGluAlaLysGluAla	REFERENCY
QΩ		AUTHOR
δλ	oo ot	TITLE
Ф	381 IGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAAGACCCTTGAAAGCT 440	JOURNAI
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දු පු	101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120 	COMMENT
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δ	141 ProGlullelleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr 160	
Пb	621 CCAGAAATTATCACCACCACGAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAA	
à t	GluPhelleValSerAbgpSerThrTvrSerValAlaSerProTyrSerThr1leProAla	
Q C	681 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTGCAATACCTGCC 740	ORIGIN
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qq	861 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 920	λō
ζŏ	241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260	qu
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ò	261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280	ପ୍
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٥y	281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300	qu
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AK075443 1755 bp mRNA linear PRI 03-SEP-2002 Homo sapiens cDNA PSEC0135 fis, clone PLACE1004850, highly similar to Homo sapiens lymphatic endothelium-specific hyaluronan receptor LYVE-1 mRNA.

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Direct Submission
Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory: 0.532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.)2p, Tel:81-438-52-3975, Fax:81-438-52-3986)
HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing: Helix
Research Institute (supported by Japan Key Technology Center etc.);
cDNA library construction: Institute of Medical Science, University
of Tokyo, Location/Qualifiers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                            Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K., Shii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T., Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T., HRI human cDNA sequencing project Onpublished

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Homo sapiens
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ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG
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   ProthrthrthrtproproblaproAlaSerThrSerlleProArgArgLysLysLeulle
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1 (bases 1 to 2029)
Daniel, S., Gilmore, J., Stuart, S.G. and Detection of altered expression of gent proliferation
Patent: US 6368794-A 13 09-APR-2002;
Location/Qualifiers
1. .2029
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Sequence 13 from patent
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                                                                                                                                                     GlubhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
        ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
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                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Lal, P., Tang, Y.T., Gorgone, G.A., Corley, N.C., Guegler, K.J., Baughn, M.R., Akerblom, I.E., Young, J.A., Yue, H., Patterson, C., Hulman, J.L. and Bandman, O. Human Bignal peptide-containing protein Patent: JP 2002519030-A 64 02-JUL-2002; INCYTE PHARMACUTICALS INC OS Homo sapiens (human)

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RESULT 8 AX092274 LOCUS DEFINITION Sequence 5 from Patent W00116318. ACCESSION Sequence 5 from Patent W00116318. ACCESSION AX092274.1 GI:13444451 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) Mammalia; Butheria; Craniata; Vertebrata; Euteleostomi;	aton,D.I odowski, ood,W.I. ecreted he same atent: W	urce 12372,	From No.: 5.55e-127 Defight: 2572  Score: 1657.00 Matches: 322  Percent Similarity: 100.00% Mismatches: 0  Query Match: 6  DB: 6  US-10-079-111-1 (1-322) x AX092274 (1-2372)	Oy 1 MetalaargCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20	Db 220 GTCCAAGGCTCTTTGCGTGCAGAAGGCTTTCCATCCAGGTGTCAGGAGATTATGGGG 279  Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  Db 280 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCTGATTTCACAGAAGGCTGAAGGGGGCC 339	Oy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80	Oy 101 SerProAsnProLysCysGlyLysAsnGlyValLeuIleTrpLysValProVal 120	141 ProglulielleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr	Qy 181 ProThrThrThrProProAlaProAlaSerThrSerlleProArgArgLysLeulle 200
ery Matc : -10-079-	GIGCAGAAGAGCIIICCAICCAGGIGICAIGCAGAAIIIAIGGGGG 27 ysLysalaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60 AAAAGGGGAACCAGCAGAATTTCACAGAAGCTAAGGAGGCC 33 euSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80 FINITIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArglle 10	rsile        carr	580 CCAGAAATTATCACCACACAAGATCCCATATTCAACACTCAAACTGCAACACACA 161 GluPheIleValSerAspSerThrTyrSerValalaSerProTyrSerThrIleProAla	Qy 181 ProThrThrThrProProAlaSerThrSerIleProArgLySLySLeuile 200	21 GludsniyshlapheLysasnGludlaAlaGlypheGlyGlyValProThrAlaLeu 24	Db 880 CTAGTGCTCTCCTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 939  Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetileGluThr 280  Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetileGluThr 280  Db 940 AGGTATGTGAAGGCCTTTTACAAACAAGAATCAGCAAAGGAAATGATGATGAAACC  Qy 281 LysYalValLysGluLysAlaSnAsnAsnArcAANDFroAsnGluGAACC  Qy 281 LysYalValLysGluLysAlaSnAsnAsnAsnAsnGluGASTLysThr 300	Db         1000 AAAGTGAAAGGAGAGAGAGACCATGATGATGAGAATGAGAAAACT           Oy         301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValaxGYsLeuGluAla         320           Db         1060 GATAAAAACCAGAAGAGTCCAAGAGCAAAACTACCGTGCGATGCCTGGAAGCT         1119           Oy         321 GluVal         322           Db         1120 GAAGTT         1125	115005 0711

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Oy  201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluThrGluProPheVal 220	SULT 11 6496769  SULT 11 6697609  AX697609  AX697609  AX697609  AX697609	Qy 1 MetalaargCysPhesSerLeuValLeuLeuThrSerlleTrpThrThrArgLeuLeu 20
ACCESSION  WEXYORDS  SOURCE  Homo sapiens (human)  ORGANISM  Homo sapiens (human)  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  AUTHORS  Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters, Gurney,A.L., Hillan,K.J., Marsters, Gurney, Gurney,A.L., Hillan,K.J., Marsters, Gurney,A.L., Hillan,K.J., Marsters, Gurney,A.L., Hillan, Marsters, Gurney,A.L., Hillan, Marsters, Gurney, Gur	### Socres:    3.566-127   Matches: 322   1657.00   Matches: 322   1657.00   Matches: 322   100.00\$   Conservative: 0   Info.00\$   Mismatches: 0   Info.00\$	Oy Ibl Cauthellevalsekabserini. Yesivalalaserini. Intervala 1800  640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTACAATACTGCC 699  Qy 181 ProfhrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuile 200

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Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.
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Zheng,J. and
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  Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D.,
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60/066120,21-NOV-1997
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1. 2372
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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GENENTECH INC
OS Homo sapiens (human)
PN JP 2002223786-A/165
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Best Local Similarity:
Query Match:
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                                                    TITLE
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BD172392.
BD172392.1 GI:28413692
JP 2002223786-A/165.
Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                               ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
                                                                                                   CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
                                                                                                                                   SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal
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       IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21,
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         Zheng, J.
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Matches:
Conservative:
Mismatches:
                                                                       Patent: JP 2002238586-A 165 27-AUG-2002;
GENENTECH INC
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     Goddard, A.,
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/db_xref="taxon:9606"
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                                                                                                                 Homo sapiens (human)
JP 2002238586-A/165
27-AUG-2002
18-DEC-2001 JP 200138
17-SEP-1997 US 60/
       Gurney, A.L.,
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   Wood, W.I.,
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Best Local Similarity:
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                           fuan, J
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2372)
11eThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
                                                                       CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
                                                                                                             TGTAGGCTGCTGGGACTAGGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
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JP 2002238586-A/165.
Homo sapiens (human)
Homo sapiens
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KEYWORDS
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C12P21/02,C12P21/08//(C12P21/02,C12R1:91),(C12P21/02,C12R1:19), PC (C12P21/02,C12R1:645),C12N15/00,C12N5/00,C12N15/00 CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the
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C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10,
                                                       Zheng, J. and
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dammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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60/059117
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/organism='Homo sapiens (human)'.
                             1 (bases 1 to 2372)
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D.,
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Matches:
Conservative:
Mismatches:
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60/065846,18-NOV-1997 UG
60/066120,21-NOV-1997 UG
60/066772,24-NOV-1997 UG
60/066772,24-NOV-1997 UG
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60/063732,31-OCT-1997
60/063870,03-NOV-1997
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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OS Home sapiens (human)
PN JP 200223857-A/165
PD 27-AUG-2002
PP 18-EDEC-2001 JP 2001385248
PR 17-SEP-1997 US 60/059115
17-SEP-1997 US 60/059122,17-SI
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Search completed: September 15, 2004, 15:38:23 Job time : 4695 secs Н

Scoring table:

Minimum DB Maximum DB

score:

Title: Perfect

Sequence:

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Run on:

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sequence 200, App Squence 200, App Squence 200, App Squence 200, App Guence 200, App Guence 200, App Unence 20
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CRGANISM: Homo sapiens
FRATURE:
NAME/KEY: misc_feature
COTHER INFORMATION: Incyte ID No. US20030124543A1 3044710CB1
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        US-09-909-320-200

US-09-909-320-200

US-09-905-853-200

US-09-905-853-200

US-09-907-824-200

US-09-907-824-200

US-09-907-824-200

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US-09-904-553-200
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US-09-902-713-200
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Publication No. US20030124543A1
GENERAL INFORMATION:
APPLICANT: Straet, Susan G.
TITLE OF INVENTION: BREAST CANCER MARKER
FILE REFERENCE: PC-0053 CIP
CURRENT APPLICATION NUMBER: US/10/079,111
CURRENT FILING DATE: 2002-02-20
PRIOR FILING DATE: 1999-01-15
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LENGTH: 2029
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                  nucleic search, using frame_plus_p2n model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
                                                                                                                                                                                               Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
                                                                                                                                                                                                                                         Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                              Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                 Fong, Shermang Cao, Wei-Qiang
                                                                                                                                   APPLICANT: Genentech, Inc
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                                               1143 GAAGTT 1148
                         322
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                      GluVal
                                                                      RESULT 2
US-09-909-320-200
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                   542
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                                                                                                                                             ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
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                                                                                                                                                                                                                                                                                        483 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
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100.00%
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Best Local Similarity:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPRENCE: 10466-14

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic CURRENT APPLICATION NUMBER: US/09/909,320

CURRENT FILIGD DATE: 2002-01-04

PRIOR PILIGD DATE: 2000-02-22/080/04414

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILIGD DATE: 1999-07-28

PRIOR PILIGD DATE: 1999-07-28

PRIOR PILIGD DATE: 1999-07-28

PRIOR PILIGD DATE: 1999-07-28

PRIOR PILIGD DATE: 1999-09-08

PRIOR PILIGD DATE: 1999-09-09

PRIOR PILIGD DATE: 1999-09-09

PRIOR PILIGD DATE: 1999-09-09

PRIOR PILIGD DATE: 1999-09-09

PRIOR PILIGD DATE: 1999-09-13/US99/21547

PRIOR PILIGD DATE: 1999-10-05

PRIOR PILIGD DATE: 1999-11-29

PRIOR PILIGD DATE: 1999-12-16

PRIOR PILIGD DATE: 1999-12-16
Sequence 200, Application US/09909320
Patent No. US20020132240A1
GENERAL INFORMATION:
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940 AGGIAIGIGAAGGCCIICCCIIIIACAAACAAGAAICAGCAGAAGGAAAIGAICGAAAC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                       LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
                                                                        1000 AAAGTAGTAAAGGAGGAGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/909,088B

CURRENT FILING DATE: 2001-07-18

PRIOR PLING DATE: 2000-02-22

PRIOR PLING DATE: 2000-02-22

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/2009

PRIOR APPLICATION NUMBER: PCT/US99/210-09

PRIOR APPLICATION NUMBER: PCT/US99/210-09

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-29

PRIOR PLING DATE: 1999-10-5

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28514

PRIOR PLING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28514

PRIOR PLING DATE: 1999-11-29

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PRIOR APPLICATION NUMBER: PCT/US99/28514

PRIOR PLING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28514

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-20
                                                                                                                                                                                                                                                                                                                 ; Sequence 200, Application US/09909088B
; Patent No. US20020146709Al
; GENERAL INFORMATION:
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Gerritsen, Mary E.
Goddard, A.
Goddwski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Betstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER 0F SEQ ID NOS: 423
SEQ ID NO 200
LENGTH: 2372
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CURRENT FILING DATE: 2001-07-12
PRIOR PAPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 12009-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-05
PRIOR PAPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PAPLICATION NUMBER: US 60/146,222
PRIOR PAPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PAPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 200, Application US/09905291A Patent No. US20020160374A1 GENERAL INFORMATION: APPLICANT: Genentech, Inc.
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Gerritsen, Mary E.
Goddard, A.
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Mather, Jennie P.
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Botstein, David
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
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; ORGANISM: Homo sapiens
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Best Local Similarity:
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APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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                                           CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
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APPLICANT: Gao, Wei-Giang
APPLICANT: Gerner, Hanspeter
APPLICANT: Gerner, Mary E.
APPLICANT: Gerners, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gimaldi, Christopher J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pon, Jenes
APPLICANT: Pon, Jenes
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
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Best Local Similarity:
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ORGANISM: HOMO
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                                        GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Stewart, Timothy A.
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Goddard, A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Tumas, Daniel
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Eaton, Dan L.
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Indels:
     PRIOR FILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-15

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-16

PRIOR PILING DATE: 1999-12-20

PRIOR PILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

CAPPE: DNA

ORGANISM: Homo Sapien

US-09-902-962-853-200
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      SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
                          AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTTGTGTTTTGGAAGGTTCCAGTG
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Fublication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Betsein, David
APPLICANT: Betsein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Firvaroff, Ellen
APPLICANT: Firvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Garber, Hanspeter
APPLICANT: Gacher, Hanspeter
APPLICANT: Gacher, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Goddard, A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Olang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Paoni, Nicholas F.
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PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-29
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US-09-907-824-200
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Percent Similarity: 1
Best Local Similarity: 1
Query Match: 9
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Publication No. US20030003530A1
GENERAL INFORMATION:
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Botsoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, D. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreteed and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreteed and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
FILE REPERRANCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/097,841
CURRENT APPLICATION NUMBER: US/06/143,048
FRIOR FILING DATE: 1999-07-26
FRIOR FILING DATE: 1999-07-26
FRIOR PILING DATE: 1999-07-26
FRIOR PILING DATE: 1999-09-05
FRIOR APPLICATION NUMBER: PCT/US99/20594
FRIOR FILING DATE: 1999-09-08
FRIOR FILING DATE: 1999-09-08
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-00-08
FRIOR FILING DATE: 1999-10-05
FRIOR FILING DATE: 1999-10-05
FRIOR FILING DATE: 1999-11-29
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; ORGANISM: Homo sapiens
US-09-907-841-200
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US-09-906-742-200
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       INVENTION: Secreted and Transmembrane Polypeptides and Nucleic INVENTION: Acids Encoding the Same
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TITLE OF INVENTION: Secreted and Transmembran TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/904,011
PRIOR FILING DATE: 2001-07-11
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
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PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
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PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
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ORGANISM: Homo Sapien
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Best Local Similarity:
Query Match:
DB:
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US-09-904-011-200
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                                                                                        SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
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Fublication No. US20030023054A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bothkenazi, Avi
APPLICANT: Bothkenazi, Avi
APPLICANT: Bothkenazi, Avi
APPLICANT: Betrein, David
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, A.
APPLICANT: Gurney, Austin L.
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1060 GATAAAAACCCAGAAGAGCCCAAGGAAAACTACCGTGCGATGCCTGGAAAGT 1119
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    220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
                                                                        41 IleThrLeuValSerLysLysBlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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Publication No. US20030027143A1
GENERAL INFORMATION:
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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                                                                             APPLICANT: Paoni, Jumes
APPLICANT: Paoni, Juned
APPLICANT: Stewart, Timotry A.
APPLICANT: Stewart, Timotry A.
APPLICANT: Stewart, Timotry A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane F
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERRENCE: 10466-136
FILE REPERRENCE: 10466-136
FRICK PILING DATE: 2000-03-18
FRICK RILING DATE: 1999-07-26
FRICK APPLICATION NUMBER: US 60/145,698
FRICK RILING DATE: 1999-07-26
FRICK APPLICATION NUMBER: DCT/US99/20594
FRICK RILING DATE: 1999-07-26
FRICK APPLICATION NUMBER: PCT/US99/21090
FRICK APPLICATION NUMBER: PCT/US99/21090
FRICK APPLICATION NUMBER: PCT/US99/21090
FRICK RILING DATE: 1999-09-15
FRICK RILING DATE: 1999-09-15
FRICK RILING DATE: 1999-09-15
FRICK RILING DATE: 1999-11-20
FRICK RILING DATE: 1999-12-06
FRICK REPLICATION NUMBER: PCT/US99/30991
FRICK RILING DATE: 1999-12-06
FRICK REPLICATION NUMBER: PCT/US99/30991
FRICK RILING DATE: 1999-12-06
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Hillan, Kenneth, J
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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; ORGANISM: Hom
US-09-906-742-200
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                                                                                                               ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
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                                                                                                                                                                               280 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
                                                                                                                                                                                                                                340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAAACAGCCTTGAAAGGT
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                                                              MetalaargCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu
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Mismatches:
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                                                                                      Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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1657.00
100.00%
100.00%
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                            Williams, P. Mickey Wood, William, I.
                                                                                                                                                                                      Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                 Gerber, Hanspeter
Gerritsen, Mary E
                                                                                                                                                                             Paoni, Nicholas F.
                                                                                                                                         Kljavin, Ivar J.
Mather, Jennie P.
                                                                           Goddard, A.
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ORGANISM: Homo Sapien
US-09-906-838-200
                                                                                                                                                                Pan, James
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                                                 APPLICANT:
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1657.00
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ORGANISM: Homo sapiens
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Best Local Similarity:
    ; ORGANISM: Homo
US-09-907-613-200
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                             Sequence 200, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bettein, David
APPLICANT: Eaton, David
APPLICANT: Eaton, Dan L
                                                                                                                                                                                                  Ferrara, Napoleone
Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Matches:
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
PRIOR FILING DATE: 2000-01-05
SEQ ID NO 200
LENGTH: 2372
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Best Local Similarity:
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                         1060 GATAAAAACCCAGAAGAGTCCAAGAACAAAAACTACCGTGCGATGCCTGGAAGCT 1119
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APPLICANT: Stewart Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Word William, P. Mickey
APPLICANT: Word William, P. Mickey
APPLICANTON NOMER: US/09/07,942
CURRENT APLICATION NOMER: US/09/07,942
CURRENT APLICATION NOMER: US/01/45,048
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
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PRIOR PLING DATE: 1999-01-08
PRIOR PLING DATE: 1999-01-08
PRIOR PLING DATE: 1999-01-08
PRIOR PLING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: PCT/US99/28014
PRIOR PLING DATE: 1999-10-06
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-06
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-11-06
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/30095
      AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
                                                                                                                                                                                                       Sequence 200, Application US/09907942
Publication No. US20030027146A1
GENERAL INFORMATION:
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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PRIOR APPLICATION NUMBER: PCT/US99/28313  PRIOR FILING DATE: 1999-11-30  PRIOR PLING DATE: 1999-11-30  PRIOR FILING DATE: 1999-12-02  PRIOR PILING DATE: 1999-12-02  PRIOR PLING DATE: 1999-12-02  PRIOR PLING DATE: 1999-12-06  PRIOR PLING DATE: 1999-12-16  PRIOR PLING DATE: 1999-12-20  PRIOR PLING DATE: 1999-12-20  PRIOR PLING DATE: 1999-12-20  PRIOR FILING DATE: 2000-01-05  TYPE: DAA  CRANISM: HOMO Sapien  US-09-904-859-200	Alignment Scores:     2.23e-188		Qy	Oy 101 SerProAsnProLysCysGlyLysAsnGlyValCeulleTrpLysValProVal 120  460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCCTGATTTGGAAGGTTCCAGTG 519  Oy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  bb 520 AGCCGACGTTTGCAGCCTATTGTTACACCTATCTGTACTTGGACTTGTGTTTTTTTT	Qy         161 GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180           Db         640 GAATTTATGCGGTGACGTACCTACTCGGTGGCATCCCTTACTCTACATACCTGCC 699           Qy         181 ProThrThrThrProProAlaBerThrSerIleProArgArgLysLeuile 200           Db         700 CCTACTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCACGAGAAAAATTGATT 759           Qy         201 Cy8ValThrGluValPheMetGluThrSerThrMetSerThrGluT
Oy 261 ArgTyrValLysAlaPheProPherhrAsnLysAsnGlnGlnLysGluMetileGluThr 280	APPLICANT: Genentech, Inc. APPLICANT: Ashkenazi, Avi APPLICANT: Botherin, David APPLICANT: Baton, David APPLICANT: Baton, Dan L. APPLICANT: Ferrara, Napoleone APPLICANT: Filvaroff, Ellen APPLICANT: Fong, Sherman APPLICANT: Gao, Wei-Qiang	APPLICANT: Gerber, Hanspeter; APPLICANT: Geriber, Mary E. APPLICANT: Goddard, A.; APPLICANT: Godweki, Paul J. APPLICANT: Grimaldi, Christopher J. APPLICANT: Hillan, Kenneth, J. APPLICANT: Hillan, Kenneth, J. APPLICANT: Milan, Ivar J. APPLICANT: Mather, Jennie P.	APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Pani, Nicholas F. APPLICANT: Roy, Margaret Ann APPLICANT: Tumas, Daniel APPLICANT: Williams, P. Mickey APPLICANT: Wood, William, I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14 GURRENT APPLICATION: DANE: US/09/904,859 GURRENT APPLICATION: DANE: 2001-07-17	PRIOR APPLICATION NUMBER: 09/665,350 PRIOR FILING DATE: 2000-09-18 PRIOR PLING DATE: 2000-09-18 PRIOR APPLICATION NUMBER: PCT/US00/04414 PRIOR APPLICATION NUMBER: US 60/143,048 PRIOR APPLICATION NUMBER: US 60/145,698 PRIOR PLING DATE: 1999-07-07 PRIOR FILING DATE: 1999-07-26 PRIOR FILING DATE: 1999-07-26 PRIOR APPLICATION NUMBER: US 60/146,222 PRIOR PLING DATE: 1999-07-28 PRIOR PLING DATE: 1999-07-28 PRIOR PLING DATE: 1999-07-28	PRIOR FILING DATE: 1999-08

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Percent Similarity:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
                                                               820 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCCACGGCTCTG
                                                                                                                              880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA
                                                                                               LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
                                                                                                                                                              ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
                                GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
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CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: EXT/USO0/04414
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 1099-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
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PRIOR PELING DATE: 1999-09-08
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Publication No. US20030036061A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fivaroff, Ellen
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Goddard, A.
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Gao, Wei-Qiang
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PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-10-05
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-20
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APPLICANT: Goldard, Paul J.
APPLICANT: Goldward, Paul J.
APPLICANT: Gurmey, Austin L.
APPLICANT: Gurmey, Austin L.
APPLICANT: Gurmey, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Mather, Jenne P.
APPLICANT: Mather, Jenne P.
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,820
CURRENT PILING DATE: 2001-07-13
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
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                                                                                                                181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLySLySLeuIle
                                                                                            CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerfitsen, Mary E.
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20544
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
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SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
              CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
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Search completed: September 15, 2004, 21:23:14 Job time: 593 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

September 15, 2004, 13:19:40 ; Search time 3066 Seconds (without alignments) 3136.211 Million cell updates/sec 1 MARCFSLVLLLTSIWTTRLL......NPEESKSPSKTTVRCLEAEV 322 US-10-079-111-1 1657 Perfect score: Sequence: Run on:

0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table:

27513289 segs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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em\_gss\_vrc. em\_gss\_phg:\* em\_gss\_vrl:\* gb\_gssl:\* em\_gss\_mus:\*
em\_gss\_pro:\*
em\_gss\_rod:\* em\_gss\_fun:\* em\_gss\_mam:\* em\_estom:\* em\_gss\_hum:\* em gss inv:\* em\_gss\_pln:\* em\_estba:\*
em\_esthum:\*
em\_esthum:\*
em\_esthun:\*
em\_estro:\*
gb\_est1:\*
gb\_est1:\*
gb\_est4:\* em\_estfun:\* gb\_est5:\* EST: \* Database :

gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description		SOCIA ALGOODI	20021 AL33002	32233 AU33223	0 PI.5510	53858 ALS5385	459046 BX4590	366718 BX36671	50911 AL55091	19512 AL54951	74 AL54387	17774 ALS4777	52127 AL55212	402505 BX4025	4430 AL544430	6589 BX3665	661 AL55266	829 AL55082	217 AL54621	615 AL55061	623 AL54662	777 AL552777	1420 603044	331	472	980	865	٦ ٢	, ,	3354 60250422	56260 602585	16199	704927	46671	3994314	46565 7	229605 AGENCOUR	763579 6	04417 A	33920 AL	07758 100390	0966 Shult	988195 A	9328 yu19a09
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## ALIGNMENTS

AL550279 Homo sapiens PLACENTA COT 25-NORMALIZED Homo Sapiens CDNA CLONE CSODI039YJ06 5-PRIME, mRNA sequence. Homo sapiens
Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1154) AL550279.2 GI:31272096 RESULT 1 AL550279 LOCUS DEFINITION SOURCE ORGANISM ACCESSION VERSION KEYWORDS

REFERENCE

721

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1022 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT 1081
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COT 25-NORMALIZED Homo sapiens CDNA
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
http://www.genoscope.cns.fr/
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=cS0DI058DG07QPl&cluster=5952.r. Contact :
Feng Liang Email : fliang@llfetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI058DG07QPl.
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/db xref="t-xon:9606"
/clone="CSODIO58YN14"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
                                                                                                                                                                                                                                                        GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
                                                                                                                                                                                                                                                                                       GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCCACGGCTCTG
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                                                                        ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
                                                                                                                                                               CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                                                                                                                                                                                              TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
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  GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
                                                                                                CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Ombublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12887768.
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clone CS0D1058YN14 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Email: segref@genoscope.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI039DE03QPl&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI039DE03QPl.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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                                                                          gi:12887098
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 15, 2001 this sequence version replaced contact: Genoscope
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Db   998 MAAGTAGTAAAGGAGAAAGGCCAATGATWASCACCCYAATGAGGATCAAAGAAACT 1057   Qy	1015 bp mRNA 552299 Homo sapiens PLACENTA COT 25-NORM cone CSOD1069YN02 5-PRIME, mRNA sequence. 552299	_	REFERENCE 1 (bases 1 to 1015) AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D. TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished (2001) COMMENT On Feb 15, 2001 this sequence version replaced di.12891068		Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see	http://www.genoScope.cns.rr/ cgi-bin/cluster.cgi?seq=CSODI069DG01QP1&cluster=5952.r. Contact : Feng Liang Email : fliangblifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600	FEATURES Faraday Avenue Genoscope sequence ID : CSODIO69DGGIQPI.  Source 11015 /organism="Homo sapiens"	/mol type="mRNA" /db_xref="taxon:9606" /clone="CS0D1069yN02" /tissue_type="PLACENTA COT 25-NORMALIZED"	/clone_ilb="Homo sapiens PLACENTA COT 25-NORNALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V	Sires of the pumyspoki & Vector. Library was normalized. Inment Scores:	1.9e-126 1480.00 1arity: 100.00% imilarity: 100.00%	indels: Gaps: 9 (1-1015)	Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20	Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40	Qy       41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla       60         Db       264 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC       323	Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	50 Matches: 1201 50 Matches: 296 Conservative: 3 Mismatches: 11 78 Indels: 3 Gaps: 1	1 (1-322) x ALS50621 (1-1201)  MetAlaArgCysPheSerLeuValLeuLeuLeuLhrSerlleTrpThrThrArgLeuLeu 20	aGluGluLeuSerlleGlnValSerCysArglleMetGly 40 	luala 60       AGGCC 337	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80 	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle 100 	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120	SerargdinphealaalaTyrCysTyrasnSerSeraspThrTrpThrasnSerCysIle 140 	ProgluilellethrThrLysAspProilePheAsnThrGinThrAlaThrGinThrThr 160 	GluphellevalSerAspSerThrTyrSerValAlaSerProTyrSerThr1leProAla 180 :::	aproalaserThrSerIleProargArgLysLysLeuIle 200	ysvalThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220	GluksniysalaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240 	LeuvalLeuvlalaLeuleuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVallys 260 	ProPheThrAshLysAsnGlnGlnLysGluMetIleGluThr 280 	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
	Alignment Scores: 3.64e Pred. No.: 1510 Score: Bercent Similarity: 95.5: Best Local Similarity: 94.5: Query Match: 91.16	US-10-079-111-1 (1-322) x AL: QY	21 ValGinGlySerLev 	41 IleThrLeuvalSen 	61 CysArgleuleuGl) 	81 SerPheGluThrCys 	101 SerProAsnProLys	121 SerargglnPheala 	141 ProGlullelleTh: 	161 GluPhelleValSer :::           638 AAATTTATTGTCAGT	181 ProThrThrThrProProAl 	201 CysValThrGluVal 	Oy 221 Gludsniysaladla 	241 LeuValLeuAlaLeu 	261 ArgTyrVallysAlaPhe 	281 LysValValLysGlı 

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GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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http://fulllength.invitrogen.com/
Faraday Avenue Genoscope sequence
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                                                                                     /organism="Homo
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I (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12880008.

Contact: Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

BP 191 91006 BYRY cedex - France

Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5952.r For

more information about this cluster, see

http://www.genoscope.cns.fr,

cgi.bin/cluster.cgi?see_CSOD1029CE05QPl&cluster=5952.r. Contact:

Feng Liang Email: fliang@lifetech.com URL:
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                                                                   AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGATGGATTCGTGGTCATCTCTAGGATT 443
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Catarrhini, Hominidae, Homo.
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                                         SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValUeSerArglle
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AUTHORS
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241 LeuValLeuAlaieuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVallys 260	Qy 21 ValGlnG	ValGlnGlySerLeuAr
846 CTAGTGCTTGCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 905	Db 158 GTCCAAC	Grccaaggcrcrrrgcg
261 ArgTyrVallysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMet1leGluThr 280	Qy 41 IleThrL	LeuValSerLy
906 AGGTATGTGAAGGCCTTCCCTTTTACAAACAATCAGCAGAAGGAAATGATGGAAACC 965	Db 218 ATCACCC	ATCACCCTTGTGAGCAA
281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300	Qy 61 CysArgI	CysArgLeuLeuGlyLe
966 ACAGTAGTAAAGGAGGR-GAGGGCAATGATAGCAM-CCTAATGRGGATCAAAGAAACT 1021	 Db 1GTAGGC	TGTAGGCTGCTGGGACT
301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGlu 319	Oy 81 SerPhec	SerPheGluThrCysSe
1022 GATAAAA-CCAGAAGACCCAGAGTCCAGCAAACTTMCGTGCGATGCTCGGAG 1074	Db 338 AGCTTTG	AGCTTTGAAACTTGCAG
RESULT 5 A1.55.1020	Oy 101 SerPro	SerProAsnProLysCy
LOCUS AL551020 1201 bp mRNA linear EST 31-MAY-2003 DEFINITION AL551020 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA	Db 398 AGCCCAA	AGCCCAAACCCCAAGTG
clone CSODIO66YL13 5-PRIME, mRNA sequence.	Qy 121 SerArg	SerArgGlnPheAlaAl
	Db 458 AGCCGAC	AGCCGACAGTTTGCAGC
Σ	Oy 141 ProGlul	ProGlullelleThrTh
	Db 518 CCAGAAA	CCAGAAATTATCACCAC
	Qy 161 GluPhel	GluPheIleValSerAs
	Db 578 GAATTA	GAATTTATTGTCAGTGA
	Oy 181 ProThr1	ProThrThrThrProPr
Genoscope - Centre National de Sequencage	Db 638 CCTACTA	CCTACTACTACTCCTCC
ref@genoscope.cns.fr, Web : www.genc	Qy 201 Cysvall	CysValThrGluValPh
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For	 Db 698 TGTGTCA	
<pre>more intormation about this cluster, see http://www.genoscope.cns.fr/</pre>	Qy 221 GluAsnLy	LysAlaAlaPh
cgi-bin/cluster.cgi?seq=CSODI066CF07QP1&cluster=5952.r. Contact : Feng Liang Email : fliang@lifetech.com URL :	758	AGCAGO
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSON1066CED7001	7 1 1	o.Trio.Telfino.TeVino
FEATURES Location/Qualifiers		
' -	010	ביים ביים
/ dol_cype==mknA~ / db_xref="taxon:9606"	261	ArgTyrValLysAlaPh 
/clone="CSODIO66YL13" /tissue type="PLACENTA COT 25-NORMALIZED"	Db 878 AGGTATC	AGGTATGTGAAGGC-TT
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"	Oy 281 LysValy	LysValValLysGluGl
/more= Tak bridge of bridge with a Noticoligo(ur) priner. Five prine end enriched, double-strand cDNA was	Db 937 AAGTA-G	 
	Qy 301 AspLysA	AspLysAsnProGluGl
	   Db 993 GATAAACC	ACCAGAAG
Alignment Scores: Pred. No.: Score: 1.53e-122 Length: 1201 Score: 1439.00 Matches: 300 Percent Similarity: 94.98\$ Conservative: 3		;
CY: 74.044 Inteller: 86.84% Indelle:	<del>.</del>	HOMO Sapie
322) x AL551020 (1-1201)		AL553858.2 GI:31279
etAlaArgCysPheSerLeu	Σ	sapiens (human sapiens
	EUKALYOLA	Eukaryota, metazoa;

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1014 bp mRNA linear EST 31-MAY-2003 ens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA 5-PRIME, mRNA sequence.
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                                                    luSerLysSerProSerLysThrThrValArgCysLeuGlu 319
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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                                                     MetAlaArgCysPheSerLeuValLeuLeuIhrSerIleTrpThrThrArgLeuLeu
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271 331 391 451 100 511 120 571 140 631 160 691 180 09 80 40 20 Contact GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla ATCACCCTTGTGAGGAAAAAGGCGAAACCCGCGCAGCTGAATTTCACAGAAGCTAAGGAGGCC SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu Areaccaserreaccresrerrecrecrecrecrecareascaceasecre ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 272 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG TGTAGGCTGCTGGGACTAAGTTTGCCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT AGCCCAAACCCCAAGTGTGGGAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACAACAACA Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seque/Gegenoscope.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r F
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=cSOA1040CB02QP1&cluster=5952.r. Contac
Feng Liang Email: fliang@lifetech.com VRL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOA1040CB02QP1. 1201 260 0 14 2 Length:
Matches:
Conservative:
Mismatches:
Indels:

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AL549512
AL549512 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI044YN16 5-PRIME, mRNA sequence.
AL549512. GI:31271330
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                                                          154 Argaccaggractricagcergergractricisactriscatergraccacgaggsteetg
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db_xref="taxon:9506"

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/tissue type="PLACENTA"

/clone=12b="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."
GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
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                                             ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
                                                                                                    TGTGTCACAGAAGTTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAAACTTGTT
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi/seq-cS0D1044DG08QP1&cluster=5952.r. Contact :
Feng Liang Bmail : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1044DG08QPI.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lib="trand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BooR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 972)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12885569.
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/db_xref="taxon:9606"
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1 (bases 1 to 911)
11, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length CDNA libraries and normalization
On Peb 15, 2001 this sequence version replaced gi:12876353.
Contact: Genoscope
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
                                                          563 CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACA
                                                                                                                                  GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
                                                                                                                                                                                                                                                                                                                                          683 CCTACTACTACTCCTCCTCCTCCTCCTTCCACTTCTATTCCACGGGAAAAAATTGATT
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r F
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODIOO5AD07QPl&cluster=5952.r. Contac
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIOO5AD07QPl.
Location/Quallfiers
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/db_xref="taxon:9606"
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Homo sapiens
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1. (bases 1 to 1201)

1. Liver.C., Jessee, J. and Polayes, D.

1. Full-length cDNA libraries and normalization

1. Unpublished (2001)

2. Contact: Genoscope

3. Contact: Genoscope

3. Genoscope - Centre National de Sequencage

3. District National de Sequencage

3. District National de Sequencage

3. District National de Sequencage

4. District National de Sequencage

5. District National de Sequencage

6. District National de Sequence cluster 5952.r Por more information about this cluster, see

6. District National de Sequence cluster 5952.r Contact :

7. Feng Liang Banil : fliang@lifetech.com URL :

8. District National Genoscope sequence ID : CSODI033CBO6QPI.

9. District National Componention 1600

9. Paraday Avenue Genoscope sequence ID : CSODI033CBO6QPI.
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/db_xref="taxon:901033YD11"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/tissue_type="PLACENTA COT 25-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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25-NORMALIZED Homo sapiens cDNA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Conservative:
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Indels:
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GluPheileValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 18	863 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAGTGAACCATTGTT 922  221 GluasniysalaalaaPhelysasnGlualaalaGlygheGlyGlyValProThralateu 240  221 GluasniysalaAlaaPhelysasnGlualaalaGlygheGlyGlyValProThralateu 240  223 GAAAATAAAGCAGTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCMCG-GCTCTG 981  241 LeuValleuAlaleuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVallys 260  982 CTAGTGGTTGTTCTTCTTCTTTTTTTTTTTTTTTTTTTT	ArgTyrValLysalaPheProPheThrAsniysAsnGlnGlnLys 275  RG-TATGTAAGSCTCCCCTTTACAAMARAATMRCAGAAGG 1080  L552127  L172 bp mRNA linear EST 31-MAY-200  L552127 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  L000 CS001059YA12 5-PRIME, mRNA sequence.	S EST.  Homo sapiens (human)  ISM Homo sapiens (human)  ISM Homo sapiens  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.  ICE 1 (bases 1 to 1172)  ISS 11, W Ba. Gruber, C., Jessee, J. and Polayes, D.  Full-length cDNA libraries and normalization  AL Unpublished (2001)  On Feb 15, 2001 this sequence version replaced gi:12890728.  Genescope - Centre National de Sequencage	BP 191 91006 EVRY cedex - France Email: seqrefeganoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi.bin/cluster.cgi?seq=CSODIO59BA06Qpl&cluster=5952.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://tullength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODIO59BA06Qpl.  L. 1172	/mol type="mRNA" /db_xref="raxon:9606" /db_xref="raxon:9606" /clone="Calon1059YA12" /tissue type="PLACENTA COT 25-NORMALIZED" /clone="Tib="Homo sapiens PLACENTA COT 25-NORMALIZED" /clone="Tib="Homo sapiens PLACENTA COT 25-NORMALIZED" /clone="Tib="Fund of the placenta" /clone="Tib="Fund of the assistance of the assistance of the placenta" /clone="Tib="Tib="Tib="Tib="Tib="Tib="Tib="Tib

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                                                                                          Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
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cgi-bin/cluster.cgi?seq=CS1AI012ZA06QPl&cluster=5952.r. Contac
Reng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS1AI012ZA06QPl.
Location/Qualifiers
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Li, Ubases I to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-Length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12876910.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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cgi.bin/cluster.cgi?seq=CSGDIO18BD06QPl&cluster=5952.r. Contact
cgi.bin/cluster.cgi?seq=CSGDIO18BD06QPl&cluster=5952.r. Contact
Feng Liang Bmail: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO18BD06QPl.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
                                                                                                752 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCAGGGAAAAAATTGATT
                                                                                                                                                                                    CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r
more information about this cluster, see
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/db_xref="taxon:9606"
/clone="CS0D1018YG12"
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US-10-079-111-1 (1-322) x AL544430 (1-1201)

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Human cDNA encoding a membrane or secretory protein clone PSEC0135.
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-MODEL=frame+ p2n.model -DEV=Xlh
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-LOOPEXT=0 -UNITS=b1ts -START=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=Dtc -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-USER=USI0079111 @CGN 1 1 470 @runat_13092004_102133_13546 -NCPU=6 -ICPU=3
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Ade71445 Human cDN
Aax52250 Protein P
Ade7850 Human PRO
Aaf72408 Human PRO
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Aaf92060 Human PRO
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Jatabase

Result No.

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Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development.
                Claim 1; SEQ ID NO 149; 609pp + Sequence Listing; English.
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This invention relates to nucleic acid sequences AAF93744 - AAF93916
which encode human secretory or membrane proteins represented by AAB88317
AAF62232 - AAF62235 which are used to isolate the CDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and CDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The cused in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The proteins/membrane polypeptides and their role in metabolism and in assays to identify modulators (agonists and antagonists of antagonists of expression and activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as therapeutic agents of diseases which may be executed include rheumatoid arthritis and diabetes

Sequence 1755 BP; 502 A; 422 C; 406 G; 425 T; 0 U; 0 Other;

1755 322 0 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 2.66e-146 1657.00 100.00\$ 100.00\$ Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Pred. No.: Score:

(1-1755)US-10-079-111-1 (1-322) x AAF93818

77 D-DT-80	T = T T T =	US-IU-U/9-III-I (I-522) X AAF938I8 (I-1755)
È	Ξ-	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerlleTrpThrArgLeuLeu 20
Ор	201 A	ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 260
ò	21 V	ValGinGlySerLeuArgAlaGluGluLeuSerIleGinValSerCysArgIleMetGly 40
qq	261 G	GTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 320
۸۵	41 I	lleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Ор	321 A	ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 380
ζζ	61 0	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
qq	381 T	
ζ	81 8	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile 100
qu .	441 A	AGCTTTGAAACTTGCAGCTATGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT 500
ð	101 8	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Ор	501 A	AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCGATTTGGAAGGTTCCAGTG 560
ò	121 8	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
ΩD	561 A	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGGATACTTGGACTAACTGGTGCATT 620
٥'n	141 P	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
q <sub>Q</sub> .	621 C	CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAA

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ò	161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
qq	681 GAATTTATTGTCAGTGACAGTACCTACGTGGGTGGCATCCCCTTACTTA
ò	181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLySLySLeuIle 200
qq	CTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAAA
δ	201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluFroPheVal 220
qq	801 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 860
ð	21 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 24
ДC	861 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 920
ò f	LeuvalLeuAlaLeuLeuPhePheGlyAlaAlaAlaAlaGlyLeuGlyPheCysTyrValLys 26
an ·	zi ciasiscilsciciccicilciilasisciscascissicilssaitiisciaiscaaa 98
ò 1	61 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
ĝ	81 AGGIATGTGAAGGCCTTCCCTTTTACAACAAGAATCAGCAGAAGGAAATGATCGAAACC 10
දු පු	281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
ò	301 AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Q	
ði	321 Gluval 322
QQ	1161
RESULT ADE7144 ID AD	ILT 2 1449 ADE71449 standard; cDNA; 2027 BP.
X X	ADE71449;
X E	29-JAN-2004 (first entry)
Z E X	Human cDNA encoding PDEBC #2.
₹₹;	breast cancer; PDEBC; metastatic; human; ss; gene.
X S	Homo sapiens.
Z Z Z	US2003124543-A1.
¥ 2.3	03-JUL-2003.
¥ £ \$	20-FEB-2002; 2002US-00079111.
¥ # \$	15-JAN-1999; 99US-00232160.
PA P	(STUA/) STUART S G. (STRE/) STREETER D G.
YY A	Stuart SG, Streeter DG;
<b>\$</b> 883	WPI; 2004-009141/01. P-PSDB; ADE71444.
T L L L	A new cDNA encoding a protein differentially expressed in breast cancer designated PCBC is useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of the disease.
X S S	Claim 2; Fig 1; 31pp; English.

us-10-079-111-1.rng

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The invention relates to an isolated cDNA encoding a protein that is differentially expressed in breast cancer, designated PDBBC. The invention is useful to diagnose breast cancer. The invention is also useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of the disease. The present sequence represents CDNA encoding human PDBBC incyte 3044710CB1. Note: There are two sequences that have been assigned SEQ ID 2 in the specification, the present sequence represents the sequence given in
                                                                                                                                                                                                                                        figure 1.
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Sequence 2027 BP; 612 A; 461 C; 445 G; 509 T; 0 U; 0 Other;

Alignment Pred. No.: Score: Percent Sin Best Local Query Match	Scores: : imilarity: ch:	3.25e-146 1657.00 100.00\$ 100.00\$	Length: Matches: Conservative: Mismatches: Indels: Gaps:	2027 322 0 0 0	
US-10-079-	111-1 (1-322)	x ADE71449 (1-	2027)		
oy Db	1 MetAlaArg            181 ATGGCCAGG	MetAlaArgCysPheSerLeuValLeuLeuLeuL 	LeuLeuLeuThrSerlle 	leTrpThrThrArgLeuLeu 	20
٨٥	21	/SerLeuArgAlaGlu	GluLeuSerIleGlnV	ValGinGiySerLeuArgAlaGluGluLeuSerIleGinValSerCysArgIleMetGly	40
Пр	241 Grecaage	rctriccicacada	kaderrrecarecade	rgrcarcagarrareee	300
75 25	41 IleThrLeu           301 ATCACCCTT	JValSerLysLysAla	AsnGlnGlnLeuAsnF 	eThrieuValSeriysLysAlaAsnGlnGlnieuAsnPheThrGluAlaLysGluAla	360
٥٧	61 CysArgieu	TheuGlyLeuSerLeu	AlaglyLysAspGlnVe	/alGluThrAlaLeuLysAla	80
qq	361 TGTAGGCTG	GTAGGCTGCGACTAAGTTTGGCCGGCAAGGA	_당		420
λ	81 SerPheGlu	luThrCysSerTyrGlyTr	TrpValGlyAspGlyPhev	heValValIleSerArgile	100
Db	GCTTTG	CTTGCAGCTAT	GTTGGAC		480
λō	101 SerProAsn	1ProLysCysGlyLys	AsnGlyValGlyValI	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal	120
QQ	481 AGCCCAAAC	cccaagigigigaaa	AATGGGGTGGGTGTCC	TGATTTGGAAGGTTCCAGTG	540
ζŏ	121 SerArgGlr	nPheAlaAlaTyrCys	TyrAsnSerSerAsp1	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
qq	541 AGCCGACAG	STTTGCAGCCTATTGT	TACAACTCATCTGATA	ACTTGGACTAACTCGTGCATT	009
λŏ	141 ProGluIle	roGlullelleThrThrLysAsp	eThrThrLysAspProllePheAsnThrG	snThrGlnThrAlaThrGlnThrThr	160
Db	601 CCAGAAATT	ratcaccaccaaagat	CCCATATTCAACACTC	CTCAAACTGCAACACAAACAACA	099
ò	161 GluPheile	PhelleValSerAspSerThrTyrSerValAla	TyrSerValAlaSerF	SerProTyrSerThrlleProAla	180
qq	661 GAATTTATT		TACTCGGTGGCATCC	TACCTGC	720
ογ	181 ProThrThrP	roProAla	(ProAlaSerThrSerIleF	eProArgArgLysLysLeuIle	200
Op	721 CCTACTACT	CICCIGCI	GCTTCCACTTCTATTC	CTATTCCACGGAGAAAAAATTGATT	780
ò	201 CysValThr	rGluValPheMetGl	uThrSerThrMetSerT	ThrGluThrGluProPheVal	220
q <sub>Q</sub>	781 TGTGTCACA	AGAAG	-6	TGAACC	840
λ̈	221 GluAsnLys	BAlaAlaPheLysAsn	nLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrA	3lyGlyValProThrAlaLeu	240
qa	841 GAAAATAAA	AGCAGCATTCAAGAAT	GAAGCTGCTGGTTTC	SGAGGTGTCCCCACGGCTCTG	006
λō	241 LeuValLeu	uAlaLeuLeuPhePhe	eGlyAlaAlaAlaGlyI	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
qq	901 CTAGTGCT	recretectrati	rggrgcrgcAgcrggrd	CTTGGATTTTGCTATGTCAAA	096

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
                        961 AGGIATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
                                                                   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
                                                                                                                                      AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
                                                                                                                                                         1081 GATAAAAACCCAGAAGAGTCCAAGGAAGCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT
                                                                                                      1021 AAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                               Human signal peptide containing protein HSPP-64 cDNA SEQ ID NO:198
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                                                                                                                                                                                                                                                                                                                      BP.
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98US-0094983P.
98US-0102686P.
98US-0112129P.
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01-OCT-1998;
11-DEC-1998;
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         reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's diseases, schizophrenia, ovulatory defects muscular dystrophy). HSPP mucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation amplification assays (for diagnosis and monitoring), in gene therapy, as antisense, tripler-forming or ribozyme therapeutics, for detecting related sequences or genetic or ribozyme therapeutics, for detecting related sequences or genetic expecific antibodies (Ab) and to screen for agonists and antagonists (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP competitive drug screens, and for purification of HSPP from naturals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A new cDNA encoding a protein differentially expressed in breast cancer designated PCBBC is useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of
                  GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGTTTGGAGGTGTCCCCACGGCTCTG
                                                         LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
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GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
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                        AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
                                     Protein PRO263 cDNA clone DNA34431-1171.
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                                 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
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                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens.
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 atherosclerosis; cardiac injury; infertility; premature aging; AIDS; diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.
                                                                                                                                                                                                                                                        Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                       Goddard A,
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Best Local Similarity:
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P-PSDB; ADC78521
                                                                                    WO200015796-A2.
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                                                    Homo sapiens
                                                                                                                     23-MAR-2000
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       SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile
                                                                             SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal
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                                                                                                                                                     SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCys1le
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                                                                                                                                                                                                                                                                                                GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThr1leProAla
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                                                                                                                   460 AGCCCAAACCCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
                                                                                                                                                                                       520 AGCCGACAGTITGCAGCCTATIGTTACAACTCATCTGGATACTIGGACTAACTCGTGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's disease).
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                                                                                                                                                                                                                                                                                              , Ferrara N;
n ME, Goddard A;
Kljavin IJ;
Tumas D;
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99WO-US020594.
99WO-US020944.
99WO-US021090.
99WO-US021547.
                                                                       99WO-US023089.
99WO-US028214.
99WO-US028313.
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2000WO-US000219
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Percent Similarity:
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Query Match:
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P-PSDB; AAB80247.
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Filvaroff E, F
Godowski PJ, G
Mather JP, Pan
Williams PM, W
08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
23-NOV-1999;
02-DEC-1999;
02-DEC-1999;
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20-DEC-1999;
20-DEC-1999;
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Human; ss; gene; secreted protein; transmembrane protein; antirheumatic; antiarthritic; osteopathic; sports-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthritis.
  AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGGCTCTGATTTGGAAGGTTCCAGTG
                                                                                                            AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGGTACTTGGACTAACTCGTGCATT
                                                                                                                                                                                 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
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                                                                                  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
                                                                                                                                                                                                              GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACATACTCTGCC
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97US-0064215P.
98US-0082797P.
98US-0083495P.
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22-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAAATTATGGGG
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Wood WI;
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Watanabe CK,
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01-SEP-1999; 99WO-US020111.
15-SEP-1999; 99WO-US021090.
07-DEC-1999; 99US-01694595.
09-DEC-1999; 99US-0170262P.
11-JAN-2000; 2000WS-0175481P.
11-JAN-2000; 2000WS-0175481P.
18-FEB-2000; 2000WS-0154814.
18-FEB-2000; 2000WS-0154814.
22-FEB-2000; 2000WS-019107414.
31-MAR-2000; 2000WS-019107P.
31-MAR-2000; 2000WS-019107P.
32-MAR-2000; 2000WS-019107P.
32-MAR-2000; 2000WS-019107P.
32-MAY-2000; 2000WS-019107P.
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I, Gurney AL,
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98US-0091628P.
98US-0096012P.
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98US-0090688P.
98US-0090696P.
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2000WO-US004414.
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25-JUN-1998;
25-JUN-1998;
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02-JUL-1998;
10-AUG-1998;
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04-JUN-1998
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26-AUG-1998;
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(GETH ) GENENTECH INC. 

Goddard A, Godowski PJ; Wood WI; Gerritsen ME, Watanabe CK, Eaton DL, Filvaroff E, Grimaldi JC, Gurney AL,

WPI; 2002-731348/79.

P-PSDB; ABG95853

New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis.

2; Fig 5; 399pp; English. Claim

The invention relates to an isolated secreted and transmembrane PRO CC polypeptide having 80 % sequence identity to a sequence appearing as a polypeptide having 80 % sequence identity to a sequence of an extracellular domain of the proteins with their associated signal peptide. Associated signal peptide or lackfing its associated signal peptide. Associated signal peptide crise acids encoding the proteins, wetcrox, host cells, fusion proteins are acids encoding the proteins, bost cells, fusion proteins are caids encoding the proteins, vectors, host cells, fusion proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample useful for detecting a polypeptide designated as B, B, C, Or D in a sample cample, where the formation of the Conjugate in the sample, where the formation of the Conjugate in the sample, where A is a PRO1972 polypeptide, B is a PRO2010 polypeptide, I is a PRO1975 polypeptide, B is a PRO2010 polypeptide, H is a conjugate in the sample, where A is a PRO1972 polypeptide, B is a PRO20040 polypeptide, H is a CC polypeptide, F is a PRO1975 polypeptide, B is a PRO20040 polypeptide, H is a coll suppering by a propering and I is a PRO1976 polypeptide. The sample comprises a cell suppering a polypeptide designated as A, B, C or D or E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a cell expressing the A, B, C or D polypeptide or an antibody. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule is a toxin, a radiolabel or an antibody or cell expressing a polypeptide designated as A, B, C or D or C F, G, H, or I. The cell is Rilled. The proteins are useful for modulating a polypeptide or an antidate o development and screening of therapeutic useful reagents, for chromosome dentification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant call culture natural sources. The present sequence encodes a novel secreted or transmembrane protein of the nvention

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

2372 322 0 0 0 Length:
Matches:
Conservative:
Mismatches: Indels: Gaps: 4.04e-146 1657.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores:

US-10-079-111-1 (1-322) x ABS74380 (1-2372)

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               GICCAAGGCICTITIGGGAGAGAGAGCTITCCATCCAGGTGTCATGCAGAATTATGGGG
                                                                                                                SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
                                                                                                                                                     SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
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                                                        ATCACCCTTGTGAGCGAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
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ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArglleMetGly
                                      IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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Human PRO263 cDNA sequence SEQ ID NO:31

(first entry)

16-MAY-2002

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ABL08072 to ABL080258 encode the PRO proteins given in ABB04817 to ABL0805003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides,
Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; theumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
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1, Hillan KJ, Ma
2K, Williams PM,
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2000US-0066410.
2000US-00662350.
2000US-0242222P.
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2000WO-US030873.
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2001US-00767609.
2001WO-US006520.
2001WO-US006666.
2001US-00802706.
2001US-00808689.
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2000US-0219556P.
2000US-0220624P.
2000US-0220664P.
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2000US-0222695P.
2000US-00643657.
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2001US-00866028.
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22-MAR-2001; 2
05-MAR-2001; 2
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25-MAY-2001; 2
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07-SEP-2000;
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                 a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. atherosclerosis, hypertension, arterial restenosis, rhumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polymucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention
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    proteins, agonists and antagonists are useful for treating or diagnosing
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880 CTAGTGCTTGCTCTCCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA
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AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
                                                                                                                                                                                                                                             ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTACTACTACTCCTCCTGCTCCAGCTTCCATTCCACGGAGAAAAAATTGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paoni NF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        healing. The present sequence is a coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerber H, Gerritsen ME, Goddard A;
J, Hillan KJ, Marsters SA, Pan J,
TK, Williams PM, Wood WI, Ye W;
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30-MAY-2001; 2001WO-US017443.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
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CK,
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                                                                                 GERBER H.
GERRITSEN M E.
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PAONI N F.
STEPHAN J F.
WATANABE C K.
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I, Gurney A
                                                                                                  GENENTECH INC
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                                                                                                                    BAKER K P.
FERRARA N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godowski
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11-FEB-2000;
22-FEB-2000;
       18-JUL-2001;
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The invention relates to human PRO polypeptides (secreted or transmembrane polypeptides) and the polynucleotides encoding them. The PRO polypeptides and polynucleotides can be used in treating pathological disorders and tumours, in therapeutic treatment of cardiac insufficiency disorders and tumours, in therapeutic treatment of disorders involving pathological secretion by the pancreas, including diabetes. They can also be used in treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal casions, and skin diseases associated with abnormal keratinocyte differentiation (e.g., psoriases, epithalial cancers such as lung squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas). The sequences can be used as molecular markers for protein clectrophoresis purposes and can be utilised in protein-protein binding assays, biochemical screening assays, immunoassays and cell-based assays.

This sequence represents a human PRO polynucleotide of the invention Isolated nucleic acid useful for e.g., treating pathological disorders encodes a secreted or transmembrane protein. Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI; Claim 2; Fig 73; 473pp; English. 24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
30-MAR-2000; 2000WO-US004377.
30-MAR-2000; 2000WO-US004439.
22-MAY-2000; 2000WO-US01264.
28-UJU-2000; 2000WO-US012564.
28-UJU-2000; 2000WO-US012328.
18-SEP-2000; 2000WO-US023328. (GETH ) GENENTECH INC. WPI; 2003-328338/31. P-PSDB; ABU71625 \$\text{S}\$\$

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other; 2372 322 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-10-079-111-1 (1-322) x ACA59060 (1-2372) 4.04e-146 1657.00 100.00% 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match Score:

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160 ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCCATCTGGACCACGAGGCTCCTG 219

GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG

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21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly

280 ATCACCCTTGTGAGGAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT

61

41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla

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970S-0059117P

970S-0059112P

970S-0059124P

970S-0059124P

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2000WO-US014042
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16-DEC-1999;
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05-JAN-2000;
11-FEB-2000;
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02-MAR-2000;
20-MAR-2000;
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22-MAR-2000;
22-MAR-2000;
17-SEP-1997;
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29-OCT-1997;
31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                03-NOV-1997;
07-NOV-1997;
17-NOV-1997;
18-NOV-1997;
21-NOV-1997;
24-NOV-1997;
24-NOV-1997;
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24-NOV-1997;
24-NOV-1997;
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13-SEP-1999;
15-SEP-1999;
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15-SEP-1999;
05-OCT-1999;
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01-DEC-1998;
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02-DEC-1999;
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14-SEP-1998
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                                                                                                                                                                       CCTACTACTACTCCTCCTCCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 759
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         SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
                      ACCCAAACCCCCAAGTGTGGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
                                             CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA
                                                                                                                                 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACATACTCTGCC
                                                                                                                                                                                                CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                                                                                                                                                                                                          TGTGTCACAGAAGTTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAAACCATTTGTT
                                                                                                                                                                                                                                     GluðsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
                                                                                                                                                                                                                                                GAAAATAAAGCAAGCATCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
                                                                                                                                                                                                                                                                         LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaAlaGlyLeuGlyPheCysTyrValLys
                                                                                                                                                                                                                                                                                       CTAGTGCTTGCTCTCTTTTTGTGCTGCTGCTGGTCTTGGATTTTGCTATGTCAAA
                                                                                                                                                                                                                                                                                                               ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
                                                                                                                                                                                                                                                                                                                       LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
                                                                                  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
                                                                                                                       GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted and transmembrane protein; PRO polypeptide; cancer; Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic; neuroprotective; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding human PRO polypeptide #36
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97US-0059115P.
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17-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
     AGCCGACAGTITGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
                                                                                    ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
                                                                                                                  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                760 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAAACTTGTT
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                                                                                                                                                                                         GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
                                                                                                                                                                                                                         GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
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                                                                                                                                                                                                                                                                                                                                            CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT
                                                                                                                                                                                                                                                                                                                                                                                                  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ss; gene; secreted protein; transmembrane protein; PRO; gene therapy; chromosome identification; chromosome marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA for secreted/transmembrane protein PRO263
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97US-0059121P.
97US-0059122P.
97US-0059184P.
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97US-0059115P.
97US-0059117P.
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18-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel human secreted and transmembrane proteins (PRO polypeptides), and the polynucleotide sequences are useful in molecular biology, as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide sequences may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or their antibodies are useful in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as cancer, altaheimer's disease or ischaemia, and in various diagnostic assays. The present sequence encodes a human PRO polypeptide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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, Gerritsen ME, Goddard
Hillan KJ, Kljavin IJ;
Stewart TA, Tumas D;
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Matches:
Conservative:
Mismatches:
Indels:
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2000WO-US015264.
2000WO-US020710.
2000WO-US023328.
2000US-00665350.
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P-PSDB; ABU71480.
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                           Ashkenazi A,
Filvaroff E,
Godowski PJ,
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Williams PM,
  02-JUN-2000;
28-JUL-2000;
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16-DEC-1999; 99WO-US330095.
20-DEC-1999; 99WO-US330911.
20-DEC-1999; 99WO-US330999.
05-JAN-2000; 2000WO-US003219.
11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US003665.
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20-MAR-2000; 2000WO-US005841.

20-MAR-2000; 2000WO-US008439.

22-MAY-2000; 2000WO-US014042.

22-MAY-2000; 2000WO-US015264.

28-JUL-2000; 2000WO-US020710.

24-AUG-2000; 2000WO-US023328.

18-SEP-2000; 2000US-00665350.
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970S-0063329P
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97US-0062125P.
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(GETH ) GENENTECH INC.

The invention relates to an isolated mucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of 6 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a CR secreted/transmembrane polypeptides, or PRO polypeptides or encoding a CR propertied extracellular domain. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the vector, producing a PRO colypeptide (by culturing the host cell for the expression of the PRO oplypeptide (having at least 80% sequence cell culture), an isolated PRO polypeptide (having at least 80% sequence identity to: (c) an amino acid sequence selected from the 61 PRO proteins; (b) an amino acid sequence encoded by a nucleic and molecule deposited with an ATCC number (detailed in the specification); or (c) an extracellular domain of a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide of containing the section as completed or polypeptide of tused to a percent of sequence, an anti-PRO antibody, detecting a protein of percentage and a sample suspected of containing the polypeptide.

CC peptide), a chimaeric molecule to a cell expressing a PRO245 or PRO1868 in a sample suspected of containing the polypeptide.

CC peptide, and encoded by a nucleic acids which encode PRO can be used to generate either cransgemic animals or knock-out animals which may be used to generate either transgemic animals or knock-out animals which may be used in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides and encodes may laso be used in tissue cyping.

CN PRO1900 polypeptides and undleic acids may also be used in tissue typing.

CN PRO pubpeptides are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural concres. The present sequence encodes a PRO protein. New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, in generating probes and in tissue typing. Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Amather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI; Claim 2; Fig 73; 484pp; English. WPI; 2003-329602/31. P-PSDB; ABU71926. 

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

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970S-0059113P

970S-0059117P

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                                                                                                                                                                                                                 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
                                                                                                                                                                                                                                                                                                                                   ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle
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                                                    SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
                                                                          AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTGTTTGGAATTGGAAGGTTCCAGTG
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520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
                                                                                                                                                                                            ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostic; biosensor; bioreactor; Parkinson's disease;
Alzheimer's disease; inflammation; nephritis; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human secreted and transmembrane protein PRO263 cDNA.
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Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin LJ;
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
Williams PM, Wood WI;
11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US00504.
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US008439.
30-MAR-2000; 2000WO-US014042.
02-MAY-2000; 2000WO-US015264.
28-JUN-2000; 2000WO-US015264.
28-JUN-2000; 2000WO-US015264.
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                                                                                                   (GETH ) GENENTECH INC.
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P-PSDB; ABO01809.
                                                                          24-AUG-2000;
18-SEP-2000;
                                                                                                                                                                                                                       or strokes.
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New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO335), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia

Claim 2; Fig 73; 482pp; English.

The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American C the full length coding sequence of the DNA deposited with the American C Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide comprising any of 61 sequences having 164-119 amino acids fully defined in the specification. The PRO polypeptides or polynucleotides are useful as particularly useful for detecting or treating e.g. Parkinson's disease, particularly useful for detecting or treating e.g. Parkinson's disease, althermer's disease, inflammations, nephritis, wound healing, nerve repair, collateral blood vessel formation, cancers (e.g. colorectal cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs, restenoisis, dammals (e.g. humans (e.g. keloids or scarring), ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep, pigs, agacts, or rabbits) The PRO polypeptides are useful as targets for therapeutic intervention in these diseases. The PRO polypeptides are also useful cetermination of the presence of these diseases. The PRO polypeptides are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene chocaes a novel human secreted and transmentance PRO polypeptide

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

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Т	160	21	220
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                                                                                                         September 15, 2004, 21:04:16; Search time 3065 Seconds (without alignments) 3137.234 Million cell updates/sec
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GenCore version 5.1.6
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                                                                   using frame_plus_p2n model
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8 791 12 BG485676 BG485671 8 1172 9 AL550911 AV722410 12 726 9 AV722410 AV722410 12 1201 13 BX366791 BX36679 13 1201 14 CB765478 CB76547 14 14 CB765478 CF71096 15 1201 9 AL546590 BE19867 16 299 10 BE198670 BE19867 17 227 9 AA029420 AA029420	1070 14 CB989089 CB98908 1201 9 AL570563 AL570563 420 10 BR767810 BR767810 540 12 BR767810 BR767810 978 9 AL573693 AL573693 643 13 BX114551 BX173693 1161 9 AL550876 AA347305 342 14 B93568 BA356876	1 570 10 BB611620 18 305 9 AV749159 18 1048 13 BX378468 2 973 9 AL574433 2 456 14 H93850 9 607 10 AW956729 9 12 11 12 BG173551 9 1201 9 AL571928	6 385 14 W29485 W29485 W29485 C C C C C C C C C C C C C C C C C C C	.0 642 14 CB442342 CB442342 6928	ALSS0279 ALSS0279 ALSS0279 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA ALSS0279 ALSS0279.2 GI:31272096	EST.  Homo sapiens (human)  Homo sapiens  Homo sapiens  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,  Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.  Li M.B., Gruber, C., Jessee, J. and Polayes, D.  Full-length, CDNA libraries and normalization	uppublished (2001) On Feb 15, 2001 this sequence version replaced gi:12887098. On tact: Genoscope Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see http://www.genoscope.cns.fr/	<pre>n/cluster.cgi?seq=CSODI039DE03QPl&amp;cluster=5952.r. Contact : iang Email : fliang@lifetech.com URL : /fullength.invitrogen.com/ InvitroGen Corporation 1600 y Avenue Genoscope sequence ID : CSODI039DE03QPl. Location/Qualifiers 11154</pre>
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AL546669
AL546669 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSOD1029YJ09 5-PRIME, mRNA sequence.
AL546669.2 GI:31268502
EST.
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                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       924 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
                                                                                                                                            CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
                             204 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
                                                                                                                                                                                                                                                                                                             SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
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                                                                                                                                                                SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
                                                                                                                                                                                                                                                                                                                                                                                      504 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
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El (Mases I to 1015)

Ell, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

On Feb 15, 2001 this sequence version replaced gi:12891068.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY codex - France

Bmail: seqref@genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=26001069DG01QP1&cluster=5952.r. Contact: For http://www.genoscope.cns.fr/

Faraday Avenue Genoscope sequence ID: CS0DI069DG01QP1.
                                                                                                                                                                                                                                                                                                                            AL552299
AL552299 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI069YN02 5-PRIME, mRNA sequence.
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/note="Ist strand cDNA was primed with a NotI-oligo(dT)
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                            LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
                                                                                                              962 AAAGTAGTAAAGGAGGAGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
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     ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
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Oy 201 CysValThrThrProProAlaBroAlaSerThrSerIleProArgArgLysLysLeulle 200  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  Cy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  Cy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyClyValProThrAlaLeu 240  Cy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyClyValProThrAlaLeu 240  Cy 221 GluAsnLysAlaAlaPheProPheThrAlaAlaGlyPheGlyClyClyClyClTrGTTTGTT 785  Cy 221 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyPheCysTyrValLys 260  Cy 221 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyPheCysTyrValLys 260  Cy 221 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  Cy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  Cy 262 ArgTGTGGAGGCTTCCTTTTACAACAAGAATCAGGAGAATGATCGAAAGC 965  RESULT 4  ALS51020  LOCUS  ALS51020  ALS61020  ALS6102	ACCESSION AL551020  AL551020.2 GI:31272837  KEYWORDS  EST. SOURCE  Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  Li,W.B., Gruber,C., Jessee,J. and Polayes,D. TITLE AUTHORS  Li,W.B., Gruber,C., Jessee,J. and Polayes,D. TITLE Unbublished (2001) COMMENT On Feb 15, 2001 this sequence version replaced gi:12888564. COMMENT CONTACT: Genoscope Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seque@genoscope.cns.fr Library was constructed by Life Probhologies a division of	Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSOD1066CF07QP1&cluster=5952.r. Contact :     Feng Liang Email : fliangaliferech.com URL :     http://fulllength.invitrogen.com/ InvitroGen Corporation 1600     Faraday Avenue Genoscope sequence ID : CSOD1066CF07QP1.     FATURES	
COMMENT  Contact: Genoscope  Genoscope - Centre National de Sequencage  BP 191 91006 ENYE cedex - France  BP 191 91006 ENYE cedex - France  Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr  Library was constructed by Life Technologies, a division of  Invitropen. This sequence belongs to sequence cluster 5952.r For  more information about this cluster, see  http://www.genoscope.cns.fr/  cqi-bin/cluster.ggi?seq=CSDD1029CED5CP1&cluster=5952.r. Contact :  Feng Liang Email: fliang@lifetech.com URL:  Feng Liang Email: fliang@lifetech.com URL:  Feng Liang Email: fliang@lifetech.com URL:  Raday Avenue Genoscope sequence ID: CSOD1029CED5QP1.  Location/Qualifiers  11201  AD_Aref="Laxon:9606"  AD_Aref="Texon:9606"	ent Scores: No.: t Similarit; ocal Similar Match: 1 Met R 1 Met R 1 L S ATGC 21 Valc	Iniii Inala Inala Iniii AAGCC AAGCT AAGCT FGIIe	

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GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSOIDSYPI6"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                          Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Inhalts sequence of the frachologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=cS0D1025DH08QPl&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1025DH08QPl.
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                                                   On Feb 15, 2001 this sequence version replaced Contact: Genoscope
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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                       GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
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                                                                       ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArglleMetGly
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AL546217 Homo sapiens PLACENTA COT 25-NORM clone CSODI025YP16 5-PRIME, mRNA sequence.
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle
                                                                                                           CCTACTACTACTCCTCCTCCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT
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BX455046 913 bp mRNA linear EST 22-MAY-2003
BX455046 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE011YN20
5-PRIME, mRNA sequence.
BX455046
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1 (bases 1 to 913)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
Email: sequenoscope.ons.fr. web : www.genoscope.ons.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
http://www.genoscope.ons.fr/
http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?seq=CSODE011DG10QP1&cluster=5952.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATCAGAATTATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
                                                 11eThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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850

EST 31-MAY-2003

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E I (bases I to 1014)

S Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

L Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12894087.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5952.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=cSOD1077CE09QP1&cluster=5952.r. Contact:

Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope aquence ID: CSOD1077CE09QP1.
                                                                                                                                                                                                                       AL553858 ALOMO SADIENS PLACENTA COT 25-NORMALIZED HOMO SADIENS CDNA CLODE CSODIO77XJ17 5-PRIME, MRNA SEQUENCE.
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/note="lst strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu
GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGT-CCCACGGCTCTG
                                    LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaAlaGlyLeuGlyPheCysTyrValLys
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AL553858.2 GI:31275672
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AUTHORS
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                                                                                                                            /clone="CSODEGIIN20"
/tissue type="FLACENTA"
/tissue type="FLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, wobble-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Conservative:
Mismatches:
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                       Faraday Avenue Genoscope sequence
Location/Qualifiers
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Db 282 ATCACCCTTGTGAGCAAAAAGGCGAACCAGAATTTCACAGAAGCTAAGGGCC 341  Qy 61 CysArgleuleuGlyLeuSerleuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80	Db   522 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCTT 581     Op   141 ProGluilelleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160	181 ProthrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuile	ALS44430 ALS44430.2 GI:31266274  EST.	SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Erimates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS Li,M.B., Gruber,C., Jessee,J. and Polayes,D. AUTHORS Li,M.B., Gruber,C., Jessee,J. and Polayes,D. TITLE Pull-length cDNA libraries and normalization Unpublished (2001) On Feb 15, 2001 this sequence version replaced gi:12876910. COMMENT Contact: Genoscope Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequence Email: seqref@genoscope.cns.fr Email: seqref@genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belong to sequence cluster 5952.r For	ū _

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On Feb 15, 2001 this sequence version replaced gi:12882152.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EWRY cedex - France
BP 191 91006 EWRY cedex - France
EMail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSOD1033CB060Pl&cluster=5952.r. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOD1033CB060Pl.
ALS47774 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI033YD11 5-PRIME, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                     Homo sapiens (human)
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefegenoscope.cns.fr
Initrogen. This sequence belongs to sequence cluster 5952.r. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi/seq=CSIAIO12ZA06QP1&cluster=5952.r. Contact :
Feng Liang Email : filang@alifetech.com URL :
Feng Liang Email : filang@alifetech.com VRL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSIAIO12ZA06QP1.
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1201 bp mRNA linear EST 13-MAY-2003
BX402505 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI045YA10 5-PRIME, mRNA sequence.
  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
                                                                                                                                           683 CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACAACAACAACA 742
                                                                                                                                                                                          GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-Length cDNA libraries and normalization
Unpublished (2001)
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a Not1-cligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                         743 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
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                                623 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGGGCATT
                                                                                              ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
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Conservative:
Mismatches:
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/clone="CS0D1045YA10"
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TITLE
JOURNAL
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BX402505
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KEYWORDS
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r I more information about this cluster, see this cluster, see this cluster, www.genoscope.cns.fr/cgi.bin/cluster.cgi?seq=CSODIO58CE10QP1&cluster=5952.r. Contac Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODIO58CE10QP1.
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ALSS0615 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA Clone (CSOD1058YJ19 5-PRIME, MRNA sequence.
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1. (bases 1 to 970)

1. (Jasses 1 to 970)

1. (Jasses 1 to 970)

1. (Pal. - Length c. C., Jessee, J. and Polayes, D.

Full.-length c.DNA libraries and normalization

Unpublished (2001)
                                                                                                                          ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG
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                                                                                     MetalaargCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu
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Contact: Genoscope - Centre National de Sequencage
BP 191 91006 EWRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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                                                x BX402505 (1-1201)
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1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization

Unpublished (2001)
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Contact: Genoscope
Contact: Genoscope
Contact: Genoscope
Email: Sequence Contact: France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Inbitary was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="PLACENTA COT 25-NORMALIZED"
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seqcCSOD1029AGI2QPlscluster=5952.r. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOD1029AGI2QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCT
                                                                                                                                                                              SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal
                                                                                                                                                                                                                    ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
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                                                            SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         632 CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACAACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            692 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
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                                                                                                                  452 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATTGGTGGTCATCTTAGGATT
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COT 25-NORMALIZED Homo sapiens cDNA
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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1 (bases 1 to 1201)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOAIO40CB02QPl&cluster=5952.r. Contact :
from Library Explain : fliangedifecech.com URL :
http://fulllength.invitrogen.com/!nvitrogen.com/ lovitrogen.com/ lovitrogen.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI040YD03"
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/mol_type="mixed" corrections of the property of the prime of the pr
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S Li.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Peb 15, 2001 this sequence version replaced gi:12888185.
Contact: Genoscope
Genoscope - Centre National de Sequencage
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BP 191 91006 EVRY cedax - France
Inbrary was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see
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cgi-bin/cluster.cgi?seq=CSODIO65CC11QPl&cluster=5952.r. Contac
Reng Liang Email : fliang@lifetech.com URL :
http://fullIngth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO65CC11QPl.
Location/Qualifiers
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AL552127 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSOD1059YA12 5-PRIME, mRNA sequence.
                                                                                                         200
                                eCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVa 220
                                                                                                                                                                                                                                                                             844 TTGTGTCACAGAAGTTTTTATGGAAACTAGCACMATGTCTACAGAAACTGAACCATTTGT 903
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
thtp://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODIO59BA06QPlkcluster=5952.r. Contact :
from Librang Emmil: fliang@lifetech.com URL :
thtp://tulllength.invitrogen.com/ luvitrogen.com/ luvitrogen
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                                                                                                                                                              784 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGAT
GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
                                                                                                         ProThrThrThrProProAlaProAlaSerThrSerIleProArgArg-LysLysLeu11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Li, Mass. 1 to 1172.
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
On Peb 15, 2001, this sequence version replaced gi:12890728.
Contact: Genoscope
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Indels:
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AL552127.2 GI:31273943
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E I (bases 1 to 972)

E Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

L Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12885569.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Emal: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 31-MAY-2003
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ALS49512
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                                         302 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
                                                                                                                                             362 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
                                                                                                                                                                                                                                         422 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
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JOURNAL
COMMENT
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/ione lib="NHH MGC 116"
//lone lib="Organ: pooled colon, kidney, stomach; Vector:
//lone lib="Organ: pooled colon, site_1: EncRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon, 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
                                                                                                                         BI761420 863 bp mRNA linear EST 25-SEP-2001
603044235F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5184392 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 863)
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Conne distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Flate: LLAMIL460 row.f column: 09
High quality sequence stop: 836.
Location/Qualifiers
      220 lGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValPro
                           802 IGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCM
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Matches:
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/db_xref="taxon:9606"
/clone="TMAGE:5184392"
/lab_host="DH108"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSODIO44DGO8QPl&cluster=5952.r. Contact
cgi.bin/cluster.cgi?seq=CSODIO44DGO8QPl&cluster=5952.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO44DGO8QPl.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (hases 1 to 864)

1. (hases 1 to 864)

1. (hases 1 to 804)

1. W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

On Feb 15, 2001 this sequence version replaced gi:12877812.

Contact: Genoscope
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: Sequencecope.cns.fr, whe: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODI027CB10QP1&cluster=5952.r. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI027CB10QP1.
      SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
                                          459 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
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/clone="CSODI027YD19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nin.gov

Tissue Procurement: Dr. Stefan Hanseon

clona Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

http://mage.llnl.gov

Plate: NDAM384 row: h column: 15

High quality sequence stop: 545.
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                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 760)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone lib="NIH MGC 148"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-Xhol; Site_2: BamH; Library is oligo-dT primed and directionally cloned using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-lenght clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, Mational Institutes of Health). Note: this is a NIH_MGC Library."
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Conservative:
Mismatches:
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(Dases 1 to 602)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                           AGCCCAAACCCCAAGTGTGGGAA-AATGGGGTGTCTCCTGATTTGGAAGGTTCCAGTG
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Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with ]
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lln.gov.e column: 13
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AGENCOURT 13620505 NIH MGC 148 Homo sapiens cDNA clone
IMAGE:30335820 5', mRNA sequence.
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/lab_host="DH10B TonA"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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AL552661
AL552661 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI067YG15 5-PRIME, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1116)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
20
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                                                                                                                                                                     GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
                                                                231 ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG
                                                                                                                                                                                                                                                          41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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                                                                                                                                                                                                                                                                                                      SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal
1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu
                                                                                                                                21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
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AMN46671 Soares fetal heart NDHH19W Homo sapiens CDNA clone IMAGE:376721 5' similar to PIR.A38745 A38745 cell adhesion molecule CD44 precursor - rat [1] ;, mRNA sequence.
                                                                      788 CCCTACTACTACTCCTCCTCCTGCTCCAGGCTTCCATTCCTATTCCAGGGAAAAAATTGAT 847
                                                                                                                                                             848 TIGTGTCACAGAAGTITITATGGAAACTAGCACCATGTCTACAGAAACTGAACCAITIGT 907
    128 AGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGC 787
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1 (bases 1 to 596)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulenn,M., Kucaba,T., LehM., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
Washington University School of Medicine
Mashington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
7el: 314 286 1800
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Easil: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This Consortium (info@image.llnl.gov) for further information.
Seq primar: -28M13 rev2 from Amersham
High quality sequence stop: 419.
                                                                                                                                 eCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVa
                                             aProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIl
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                                     On Feb 15, 2001 this sequence version replaced gi:12891779.

Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 ENRY cedex - France
Email: segref@genoscope.cns.fr. Neb: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=260Di067Ab08QP1&cluster=5952.r. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI067Ab08QP1.
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/clone="CSD1067Y915"

/clone lib="HOmo sapiens PLACENTA COT 25-NORMALIZED"

/clone lib="HOmo sapiens PLACENTA COT 25-NORMALIZED"

/note="lst strand cDNA was primed with a Not!-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."
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AL552777 Auco sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI068YF16 5-PRIME, mRNA sequence.
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(bases 1 to 1074)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12892000.
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                      High quality sequence stop: 456.
Location/Qualifiers
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/db_xref="taxon:9606"
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National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA inbrary Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                  80
                                                                                                                                                                          62
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                    41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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AGENCOURT 13892970 NIH_MGC 147 Homo sapiens cDNA clone IMAGE:30345877 5', mRNA sequence.
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    Conservative:
Mismatches:
Indels:
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CB988195.1 GI:30282715
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                 /tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: Sequencecope.ons.fr, www.genoscope.ons.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?seq=CSOD1068DC08QPl&cluster=5952.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1068DC08QPl.
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Matches:
Conservative:
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                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI068YF16"
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Alevano. R.
The washU-Merck EST Project
The WashU-Merck EST Project
The WashU-Merck EST Project
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 769
High quality sequence stops: 313
Source: IMAGE Consortium, Linlu
This clone is available royalty-free through LLNL
This clone is available royalty-free through LLNL
This clone is available soyalty-free through LLNL
This clone is available soyalty-free through LLNL
This clone is available soyalty for further information.
                                                                                                                                                                                                                                                            H69328 TANDA LINEAR EST 24-OCT-1995 yu19809.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:234232 5', mRNA sequence.
                                                                                                                                                                                          encoding immunogenic fragment
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases I to 465)

Hillier, L. Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Materston, R., Williamson, A., Wohldmann, P. and
                                                               IleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPhe
                                                                                         851 ATTTGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTT
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Mismatches:
Indels:
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="GDB:3787409"
/db_xref="taxon:9606"
/clone="IMAGE:234232"
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Seq primer: M13RP1
High quality sequence stop: 313.
Location/Qualifiers
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Homo sapiens
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/organism="Homo sapiens"
/mol_type="mRNA"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 368)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 24-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-GN0239-12100-341-c05&t3=2000-12-14&t4=1)
Seg primer: puc 18 forward
High quality sequence stop: 339.
                                                                                                                                                                                   61 TITATIGLOGIGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCCT 120
                                                                                                                                                                                                                                                                          121 ACTACTACTCCTCCTGCTCCAGCTTCCACTTCCACGGAGAAAATTGATTTGT 180
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                   ThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIleCys
                                                                                                                                                         PhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThr1leProAlaPro
                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone lib="GN0339"
/note="Organ: placenta_normal; Vector: puc18; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 bp mRNA linear
IL5-GN0239-141200-341-c05 GN0239 Homo sapiens cDNA,
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  Gaps:
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Email: asimpson@ludwig.org.br
                                   US-10-079-111-1 (1-322) x H69328 (1-465)
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Homo sapiens
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BG012717
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Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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602570880F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695427 5',
BG541447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 PheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIleSer 101
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 872)
                                                                                                                                                                                                                                                        2 CAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGGTGTCATGCAGAATTATGGGGATC
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.go.row: p column: 20
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tystue Procurement: cLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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487 bp mRNA linear EST 07-NOV-2002 cDNA 5, mRNA sequence.
CA407758.1 GI:24772629
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Yang, R.-Z., Shuldiner, A. and Gong, D.-W.
EST analysis of human adipose gene expression
found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Plate: LLCM1374 row: n column: 06
High quality sequence stop: 630.
Location/Qualifiers
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           /clone="InMAGE:4655427"
/lab_host="DH10B (T1 phage-resistant)"
/clonellab="NUTH MGC 77"
/lab_host="DH10B (T1 phage-resistant)"
/clonellab="NUTH MGC 77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
Sfil (ggcgcctcggcc); Site 2: Sfil (ggccattatggcc); 5 and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCCGACATG-GT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR: This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 801)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: Capabs-remail:nhh.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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DKFZp313B2422_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DKFZp313B2422_5', mRNA sequence.
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/sex="Male and Female"
/tissue type="Adipose"
/clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
/note="Vector: lambdaTriplEx"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and BST (Duesterhoeft. et al.)
        Contact: Gong Da.Wei
Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St. H4497, Baltimore, MD 21201, USA
Tel: 410 706 1622
Email: 42000@medicine.umaryland.edu
PCR PRimers
FORWARD: CTGGGAAGGGGGCCATTGTGTTGTGT
BACKWARD: AATACGACTCACTATGTGTTGG
Seq primer: GTTGGTACCCGGGAATTGG
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                                                      This is the 5' sequence of the clone insert

This is the 5' sequence of the clone insert

This is the 5' sequence of the clone insert

This is the 5' sequence of the clone insert

Clone from 5. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKE2); Email s. wiemann@dkfz- heidelberg.de;

sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing

consortium of the German Genome Project.

This clone (DKEZp11B2422) is available at the RZPD in Berlin.

This clone (DKEZp11B2422) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="313 (synonym: hlcc2)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 ATCACCCTTGTGAGGAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
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Conservative:
Mismatches:
Indels:
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Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 ValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThrAsp 301
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                                                                                                                                                                                           Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo. 1 (bases 1 to 437)
Yang, R.-Z., Shuldiner, A. and Gong, D.-W.
FET analysis of human adipose gene expression
Unpublished (2002)
Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .437

/organism="Homo sapiens"

/mol_type="mkNa"

/db xref="taxon:9606"

/dsx="Male and Female"

/tissue_type="Malpose"

/clone_lib="Human Pat Cell 5'-Stretch Plus cDNA Library"

/note="Vector: lambdaTriplEx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                 University of Maryland 660 Redwood St. HH497, Baltimore, MD 21201, USA Tel: 410 706 1672 Fax: 410 706 1622 Email: dgong@medicine.umaryland.edu
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695 GCCCTACTACTACTCCTCCTGCTCCAGCTTCCACT 730
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PER PRIMERD: CTCGGGAAGEGEGECEATTGTGTTGGT
BACKWARD: AATACGACTCACTATAGGGGGAATTGG
Seq primer: GTTGGTACCCGGGAATTC.
Location/Qualifiers
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Homo sapiens
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BX366589 1201 bp mRNA linear EST 08-MAY-2003
BX366589 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI024YP17 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO24YD17"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Est strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                      Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria; Primates; Catarrhini; Hominidae, Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDDA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323 TTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 lLeulleTrpLysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAs 133
                                                                                                                                                                                                                                                                                                           Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BRail: seqretégenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/oluster.cgi?seq-CS0A1024CH09QPl&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOA1024CH09QPl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 PheThrGluAlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 IleTrpThrThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 ValSerCysArglleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 PheValVallleSerArglleSerProAsnProLysCysGlyLysAsn-GlyValGlyVa
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95.00
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                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 473)
Yang,R.-Z.; Shuldiner,A. and Gong,D.-W.
EST analysis of human adipose gene expression
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Adipose"
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                                                                                           CB269023
473 bp mRNA linear EST 20-FEB-2(
1007930 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens
CB269023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGTTGTG 411
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                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheVal
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Conservative:
Mismatches:
Indels:
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BACKWARD: AATACGACTCACTATAGGGCGAATTGG
Seg primer: GTTGGTACCCGGGAATTC.
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/organism="Homo sapiens"
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/sex="Male and Female"
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BI763579 877 bp mRNA linear EST 25-SEP-2001
603050140F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5190393 5',
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11475 row: p column: 10
High quality sequence stop: 715.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrTrpThrAsnSerCysIleProGlullelleThrThrLysAspProIlePheAsnThr 153
strand cDNA was primed with a Not I - oligo(dT) primer [5 ApATGGARGATATTTTTTTTTTTTTTTTTTTTT 3], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not am and Eco RI sites of the modified pTYT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "
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I (bases 1 to 87).
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGAT
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/db_xref="taxon:9606"
/clone="IMAGE:5190393"
/lab_host="DH10B"
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Yj4hhll.rl Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:151365 5', mRNA sequence.
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(Dases 1 to 411)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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/lab host="DH10B (ampicillin resistant)"
/clone lib="Soares placenta ND2HP"
/note="Organ: placenta; Vector: pT773D (Pharmacia) with
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2127 Std Error: 0.00
                                                                                                                                                                      TCAAACTGCAACACAAACAGAATTTATTGTCAGTGACAGTTC-CTACTCGGTGGCAT
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           CCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGA
                                                 pThrTrpThrAsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnTh
                                                                              562 TACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACAC
                                                                                                                                              rGlnThrAlaThrGlnThrThrGluPheIleValSerAspSerThr-TyrSerValAlaS
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Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. L
Tel: 314 286 1800
Fax: 314 286 1810
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/mol_type="mRNA"
/db_xref="GDB: 56454"
/db_xref="taxon:9606"
/clone="IMAGE:151365"
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Seq puality sequence stop: 326.
High quality sequence stop: 326.
Location/Qualifiers
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/clone_ild="Nuth mac_ild"
//clote="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site 1: Not1; Site 2: ECCRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EccRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12934166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRail: sequefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODIO39DE03NP1&cluster=5952.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO39DE03NP1.
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/dlone="CSODIO39YJ06"
/tissue type="PLACENTA COT 25-NORMALIZED"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand CDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 865)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 LeuGlyPheCysTyrValLysArgTyrValLysAlaPheProPheThrAsnLysAsnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 AsnGluGluSerLysLysThrAspLysAsnProGluGluSerLysSerProSerLysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consolin cyapbe-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM425 row: a column: 11
High quality sequence stop: 687.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGENCOURT 13980091 NIH MGC_179 Homo sapiens cDNA clone CD106276
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                                             'organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-079-111-1 (1-322) x AL574194 (1-1143)
                                                                         l_type="mRNA"
xref="taxon:9606"
Location/Qualifiers
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1201)
S Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12879804.
Contact: Genoscope Genoscope - Centre National de Sequencage
BP 191 91006 ENTX redex - France
BP 191 91006 ENTX redex - France
Email: seqrefagenoscope.cns.fr web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI030AB05QP1&cluster=5952.r. Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL546565 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA Global CSD1030YC09 5-PRIME, MRNA sequence.

AL546565. GI:31268398
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/mol type="mmxn" misses
/lab xref="taxon:5944""
/lab xref="taxon:5944""
/lab host="MHGE:688206"
/lab host="MHIOB (phage-resistant)"
/lab host = 1: Sfi I;
/lab host 
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High quality sequence stop: 551.
Location/Qualifiers
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Best Local Similarity:
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   /organism="Homo sapiens"

/mol_type="mkNA"

/db_xref="Laxon:9606"

/clone="IMAGE:30366058"

/tissue_type="Pituitary"

/tissue_type="Pituitary"

/tab_host="Pituitary"

/clone_lib="NIH_MGC_179"

/clone_lib="NIH_MGC_179"

/clone_lib="NIH_MGC_179"

/clone="Organ: brain; Vector: pCWV-SPORT6.1; Site_1: EcoRV

(destroyed); Site_2: Not1; Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.1 kb. Library was

constructed by (Invitrogen). Note: this is a NIH_MGC
Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 LysGluMetIleGluThrLysValValLysGluGluLysAlaAsnAspSerAsnProAsn 294
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Eliot Spindel
cDNA Library Preparation. CLONTECH
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3127 row: p column: 04
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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1 (bases 1 to 757)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Umpublished (1997)
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Macaca mulatta
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CB229605.1 GI:28281183
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yeS2g09.rl Soares fetal liver spleen INFLS Homo sapiens CDNA clone
IMAGE:121408 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 IleSerArg1leSerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrp 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  554 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACT 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnSerCyslleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               614 AACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCA 673
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 96
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1030AB05QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The factor of th
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Unpublished (1995)
Contact: Wilson University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                             /organism="Homo
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F96904.1 GI:735528
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Fax: 314 286 1810
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COMMENT
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AUTHORS
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                                                                                               FEATURES
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/sex="male" | /sex="male" | /sex="male" | /sex="male" | /dev stage="20 week-post conception fetus" | /dev stage="20 week-post conception fetus" | /dev stage="20 week-post conception | /dev stage="10 | /dev stand conn was primed with a pac I; Site 2: Eco RI; lst stand conn was primed with a pac I - oligo-dry primer | /dev standed conn was ligated to Eco RI adaptors | /dev standed conn was ligated to Eco RI adaptors | /dev standed conn was ligated to Eco RI adaptors | /dev standed conn was ligated to Eco RI adaptors | /dev standed conn of incommalization income in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 794)

High quality sequence stops: 254 Source: IMAGE Consortium, LLNI This clone is available royalty-free through LLNI, contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1301 Std Error: 0.00
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Matches:
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/db_xref="taxon:9606"
/clone="IMAGE:121408"
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Seg primer: M13RP1
High quality sequence stop: 2
Location/Qualifiers
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Query Match:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 328)

8 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, Er., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C. (1ayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoglagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblow, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Lui, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y., Banll, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Li, Y., Bursch, C., Hungjun, J., Hudson, P., Kan, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, Hudson, P., Kan, K., Fischer, C., Hastings, G.A., Raymond, L., Wei, Y.F., Wing, J., Li, Y., Gruber, J., Husson, P., Kan, K., Fischer, C., Hastings, G., L., Kunsch, C., Hungjun, J., Li, Y., Meismer, P.S., Olsen, H., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 Argeccaegracurcagecregrangerreneaerrecareragaecaegagereerg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
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/clone lib="Embryo, 12 week II"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
XhoI"
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Contact: Kerlavage, AR
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                                                                 Contact: wooser Strangergy, Fn.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Location/Qualifiers

High quality sequence stop: 615.

Location/Qualifiers

1. .794

| Apple: "LAMASS: Town goolumn: 08 |

High quality sequence stop: 615.

Location/Qualifiers

1. .794

| Apple: "LAMAS: All 12863"

| Abb Arrayes="MRNA"

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| Abb Arrayes="MRNA"
| Adaptors were used in cloning as follows: 5' adaptor sequence: 5'-Arrayes="Contact size 1:85"

Location Arrayes and N = A, C, G, or T). Average insert size 1:85

Kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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328 bp mRNA linear EST 18-APR-1997
BET112782 Embryo, 12 week II Homo sapiens cDNA 5' end, mRNA
sequence.
AA297240.
AA297240.1 GI:1949574
Homo sapiens (human)
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     National Institutes of Health, Mammalian Gene Collection (MGC)
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                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/tissue_type="FETAL BRAIN"
/dev stage="fetal"
/dev stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCWVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                           Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 990)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 AAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGA 378
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                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSODFOOICCI2QPl&cluster=5952.r. Contac
Feng Liang Bmail : fliang@lifetech.com URL http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODFOOICCI2QPI.
Location/Qualifiers
                                                                                                                                                                                                                                                             Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequencef@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r.
more information about this cluster, see
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/clone="CSODF001YF23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 IleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValPro 119
                                                                                                                                                                                                                                                    Eukaryota...

Bukaryota...

Bukaryota...

Mammalia; Butheria Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 793)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Fodd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Feritera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,

Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 GCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGTGGATTCGTGGTCATCTCTAGG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clark.A.G. Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 AlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 AlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GCCTGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAA
                                                                                  793 bp DNA linear GSS 16-DEC
VIRTUAL TRANSCRIPT, partial sequence,
250 TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTT 291
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73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 GTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCT 220
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Mismatches:
Indels:
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Matches:
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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/gene="XLKD1"
/locus_tag="HCM4097"
                                                                                    AY411057
Homo sapiens XLKD1 gene,
                                                                                                                                genomic survey sequence.
                                                                                                                                                  AY411057
AY411057.1 GI:39767025
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22.67%
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LOCUS
DEFINITION
                                                                                                                                                                    VERSION
KEYWORDS
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ORGANISM
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                                                                                                      DEFINITION
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Pred. No.:

Score:

gene

ORIGIN

258

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25

318

65

1.05 497

RESULT 47

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/done lib="Human lris cDNA (Normalized): fg"
/clone lib="Human lris cDNA (Normalized): fg"
/note="Organ: Bye; Vector: pCMVSPORT6; A human iris
library (bx) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by Not1. This Not1 digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in virto using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(CQt 500) with 41 mg of Bio-RNA and vector blocking
oligonolocitides. The hybridized Bio-RNA/ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NIH Intramural
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 529)
Wistow, G., Bernstein, S.L., Ray, S., Wyatt, M.K., Behal, A.,
Touchman, J.W., Boulfard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of adult human iris for the NEIBank Project: steroid-response factors and similarities with retinal pigment epithelium

Mol. Vis. 8 (4), 185-195 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 ProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThrLysValValLysGluGlu 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysAlaAsnAspSerAsnProAsnGluGluSerLysLysThrAspLysAsnProGluGlu 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Section on Molecular Structure and Function National Eye Institute 6/31, NH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Blate: 03 row: c column: 09
Seq primer: M13RP1 reverse primer (ABI).
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .529
/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="fg03c09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-079-111-1 (1-322) x CD671330 (1-529)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Query Match:
DB:
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AA463325
LOCUS
                                                                 REFERENCE
                                                                                        AUTHORS
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                                                                   GSS 16-DEC-2003
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                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Pan.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
I (bases I to 70)
I (bases I to 70)
I ark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Ford, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, K.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                             790 bp DNA linear GSS 16-DEC-20
Pan troglodytes XLKD1 gene, VIRTUAL TRANSCRIPT, partial sequence,
avalle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 302 (5652), 1960-1963 (2003)
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                                                                                                                                                                                             Pan troglodytes (chimpanzee)
Pan troglodytes
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Homo sapiens (human)
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                                                                                                                                AY411058
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                                                                                   DEFINITION
                                                                                                                                                                                                               ORGANISM
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JOURNAL
                  RESULT 48
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AUTHORS
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KEYWORDS
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Lases 1 to 415)

1. (Lale, M. Le, N., Lennon, G., Marra, M., Martin, J., More, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, T., Waterston, R. and Wilson, R.

1. (Mash, Merck EST Project 1997)

1. Unpublished (1997)

1. Unpublished (1997)

1. Unpublished (1997)

1. Unpublished (1997)

1. Louis, Mo 63108

1. 414 Forest Park Parkway, Box 8501, St. Louis, MO 63108

1. 4286 1800

1. Far: 314 286 1800

1. Far: 314 280

1. Far: 314 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315 AGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTTGGAAACTTTGAAACTTTGAAACTTTGCAGC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 AlaGluGluLeuSerIleGlnValSerCysArglleMetGlyIleThrLeuValSerLys 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 LysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAlaCysArgLeuLeuGlyLeu 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAlaSerPheGluThrCysSer 86
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:6041595"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | db_xref="taxon:9606"
| clone="IMAGE:796927"
| dev_stage="8-9 weeks"
| lab_host="DH108"
IMAGE: 796927 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-079-111-1 (1-322) x AA463325 (1-415)
                             AA463325
AA463325.1 GI:2188209
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98.81%
17.08%
                                                                                                                   Homo sapiens (human)
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                                                                                                                                                Homo sapiens
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Best Local Similarity:
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DB:
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                          ACCESSION
VERSION
KEYWORDS
SOURCE
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JOURNAL
COMMENT
                                                                                                                                                                                                                          REFERENCE
AUTHORS
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Search completed: September 16, 2004, 04:48:42 Job time : 3107 secs 9/2/X

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161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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                                                                                     US-09-232-160-13
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                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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-MODEL=frame+_p2n.model -DEV=xlh
-Delograme+_p2n.model -DEV=xlh
-Q=/cgm2_1/CgpTO_sp001/US1009111/runat_13092004_102226_14021/app_query.fasta_1.519
-Q=/cgm2_1/CgpTO_sp001/US1009111/runat_13092004_102226_14021/app_query.fasta_1.519
-DB=Issued_Patents NA -QFMT=fastap -SUFFIX=0lig.rni -MINMATCH=0.1]-LCOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=0ligo -TRANS=human40.cdi
-LIST=100 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=12 -ALIGN=50 -MODE=LOCAL
-OUTRMT=pto -NORM=ext -HERPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USR=USI0079111_@CGN 1 169_@runat_13092004_102226_14021 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -SGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPERT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Appli
Sequence 12, Appl
Sequence 13, Appl
Sequence 15, Appl
Sequence 28, Appl
Sequence 28, Appl
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849, App
853, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Appl
Sequence 200, App
Sequence 200, App
                                                                                     0 ; Search time 97 Seconds (without alignments)
1842.208 Million cell updates/sec
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                                                                                                                                                                          MARCFSLVLLLTSIWTTRLL......NPEESKSPSKTTVRCLEAEV 322
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Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                        14
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                         using frame_plus_p2n model
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US-09-907-794A-200
US-09-905-125A-200
US-09-833-381-849
US-09-833-381-849
US-09-833-381-853
US-08-892-880-12
US-08-892-880-12
US-08-892-880-13
US-08-892-880-15
US-09-724-864-28
US-09-724-864-28
                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                            seqs, 277475446 residues
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                                                                                      September 15, 2004, 21:13:40
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Ygapext 60.0
Fgapext 7.0
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Perfect :
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ALTERED EXPRESSION OF GENES REGULATING CELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCTGAATTTCACAGAAGCTAAGGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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Sequence 205,
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Mismatches:
US-09-905-125A-205
US-09-902-775A-205
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Matches:
                                                                                                                                                                                                                             APPLICANT: Steve Daniel
APPLICANT: Steve Gilmore
APPLICANT: James Gilmore
APPLICANT: Susan G. Stuart
APPLICANT: Laura Stuve
TITLE OF INVENTION: DETECTION OF ALTERED EXPI
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: PA-0003 US
CURRENT APPLICATION NUMBER: US/09/232,160
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PERL PROGram
SOFTWARE: PERL PROGram
LENGTH: 2029
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                                                                                 ALIGNMENTS
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                                                                                                                                                               Sequence 13, Application US/09232160 Patent No. 6368794 GENERAL INFORMATION:
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121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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Matches:
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
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PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
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US-09-907-794A-200
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Best Local Similarity:
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                                                                                                                                                                                                                                                                     GluAsnIysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
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  GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
                                                                          ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
                                                                                                               CCTACTACTACTCCTCCTCCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT
                                                                                                                                                                         CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
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                                                                                                                                                                                                                                                                                                                      GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTG
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TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
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Sequence 200, Application US/09907794A
Patent No. 6635468
GENERAL INFORMATION:
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Godowski, Paul J.
Grimaldi, Christopher
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APPLICANT: Ashkenazi, Avi
APPLICANT: Betsein, David
APPLICANT: Betsein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Faton, Dan L.
APPLICANT: Firstara, Napoleone
APPLICANT: Firstara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT APPLICATION NUMBER: US/09/905,125A
PRIOR APPLICATION NUMBER: US/01/414
PRIOR APPLICATION NUMBER: US/01/41/416
PRIOR PILING DATE: 1099-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/28314
PRIOR APPLICATION NUMBER: PCT/US99/28314
PRIOR PELING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: PCT/US99/28314
PRIOR PELING DATE: 1999-10-20
PRIOR PELING DATE: 1999-10-20
PRIOR PELING DATE: 1999-10-20
PRIOR PELING DATE: 1999-11-20
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Best Local Similarity:
Query Match:
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US-09-905-125A-200
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Pred. No.:
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                       CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACAACAACAACA
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Patent No. 6664376
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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Williams, P. Mickey
Wood, William, I.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Mather, Jennie P.
Pan, James
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APPLICANT: ROY, MAZGREA AN APPLICANT: APPLICANT: ROY, MAZGREA AN APPLICANT: SON, MAZGREA AN APPLICANT: SERVATE, Timothy A. APPLICANT: Tumas, Danil and the APPLICANT: Tumas, P. MACKAY
APPLICANT: Tumas, P. MACKAY
APPLICANT: Wood, Milliams, P. MACKAY
APPLICANT: WOOD, MILLIAMS, D. MACKAY
APPLICANTON: Secreted and Transmembrane Polypeptides and Mucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic TITLE OF INVENTION SECRETED SON OF 10 COURTANT SELECTION NUMBER: US/09/302,775A
CURRENT FALING DARE: 2001-07-10
FRIOR PELLING DARE: 2001-07-10
FRIOR PELLING DARE: 1050-02-22
FRIOR PELLING DARE: 1050-07-20
FRIOR PELLING DARE: 1050
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                                                Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Best Local Similarity:
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US-09-902-775A-200
i Sequence 200, Application US/09902775A
i Patent No. 6686451
i GENERAL INFORMATION:
i APPLICANT: Genemech, Inc.
i APPLICANT: Botstein, David
APPLICANT: Conmovers, Avi
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Eaton, Dan L.
Ferrara, Napoleone
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Fong, Sherman
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Gerber, Hanspeter
Gerritsen, Mary E.
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; SEQ ID NO 849 ; LENGTH: 2404 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-833-381-849 Alignment Scores:	MetalaArgCysPheSerLeuValLeuLeuLeuLeu   MetalaArgCysPheSerLeuValLeuLeuLeuLeu   190 ArgGCCRGGTGCTTCAGCCTGTTTCTTCTTCT   ValGlnGlySerLeuArgAlaGluGluLeuSerI   ValGlnGlySerLeuArgAlaGluGluLeuSerI   ValGlnGlySerLeuArgAlaGluGluLeuSerI   ValGlnGlySerLeuArgAlaGluGluLeuValGalaAsnGlnGlnL	310 A-370 T	SerargGlnPhealaalaTyrCysTyrasnSerSerAspThrTrpThrAsnSerCyGTG SerargGlnPhealaalaTyrCysTyrasnSerSerAspThrTrpThrAsnSerCyGTG AGCCGACAGTTGCAGGCTATTGTAAATGCGGTGGCTGGTTTTGGAAGGTTCCAGTG AGCCGACAGTTTGCAGCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCTTT  ProGlulleIleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr  [	Oy 161 GlubhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  Db 670 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC 729  Oy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLvsLeuIle 200  T30 CCTACTACTACTCCTCCTGGTCCCAGGTTCTATTCCAGGAGAAAAATTGATT 789  Oy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  Oy 10 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  Oy 10 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 200  O CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 200  O CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 200  O CysValThrGluValPheMetGluThrSerThrMetSerThrGluThr	221 GlubanLyshlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 24
Db 280 ATCACCCTTGTGAGCAAAAGGCGGACCGGCTGAATTTCACAGAAGCTAAGGAGGCC 339  Qy 61 CysArgLeuleuGlyLeuSerLeulaGlyLySAspGlnValGluThrAlaLeuLySAla 80  340 TGTAGGCTGGAGCTGAGGACCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399  Qy 81 SerPheGluThrCySSATyrGlyTrpValGlyAspGlyPheValValIleSerArgle 100  Db 400 AGCTTTGAAACTTGCAGGTTGGAGGATGGATTCGTGGTCATCTCTAGGATT 459  Qy 101 SerProAsnProLySCySGlyLySAsnGlyValGlyValLeulleTrpLySValProVal 120  A60 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTGAAAGTTCCAGTG 519	Oy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 579  Oy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  Db S80 CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAACTGCAACAACAACAG 639  Oy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  Oy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180	1 2 2 2 2 3 3 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	820 GAAATAAAGCAGCATTCAAGAATGAAGCTGGCGGGGGGGTTGGAGTGTCCCCACGGG 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVa 880 CTAGTGCTTGCTCTCTTTTGGTGCTGCAGGTGGTCTTGGATTTTGCTATTATA 261 ArgyrValLysAlaPheProPheThrAshLysAsnGlnGlnLysGluMetIleGl 940 AGGTATGTGAAGGCCTTTCCTTTTACAAAGAATCAGCAGAAGGAAATGATCGT	OY 281 LYV81-UASHILYSELIASSALSASSASSIGLIGUESELISSELISSELISSELISSELISSELISSELISSEL	RESULT 5 US-09-833-381-849 US-09-833-381-849  S. Sequence 849, Application US/09833381  Patent No. 6672186  GENERAL INFORMATION: TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs  TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs  FILE REFERENCE: 5800-119  CURRENT FILING DATE: 2001-04-11  PRIOR APPLICATION NUMBER: 09/516,448  PRIOR APPLICATION NUMBER: 09/516,448  PRIOR FILING DATE: 2000-02-29  NUMBER OF SEQ ID NOS: 2050  SOFTWARE: FastSEQ for Windows Version 3.0

161 GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyGlyValProThrAlaLeu 240	Oy 301 AsplysAsnProGluGluSerLysSerProSerlysThrThrValArgCysLeuGluAla 320	APPLICANT: NI, JIAN APPLICANT: BENER L. APPLICANT: DILLOW, PATRICK J. TITLE OF INVENTION: CO44-LIKE PROTEIN NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, NW, SUITE 600 CITY: WASHINGTON STATE: DC COUNTRY: USA ZIATE: DC COUNTRY: USA ZIATE: COOS-3934 CONTRY: CONT	CURRENT APPLICATION COMPACTALE  CURRENT APPLICATION NAMER: US/08/82.0S  CURRENT APPLICATION NAMER: US/08/892,880  FILING DATE: HEREWITH  CLASSIFICATION NAMER: 60/021,762  PRICA APPLICATION DATA:  APPLICATION NAMER: 60/021,762  FILING DATE: 15-JUL-1996  ATTORNEY/AGENT INFORMATION:  NAME: STEFFE, ERIC K  REGISTRATION NUMBER: 36,688  REFERENCE/DOCKET NUMBER: 1488.0490001  TELEPHONE: 202-371-2600  ITELEPHONE: 202-371-2540  INFORMATION FOR SEQ ID NO: 1:
	RESULT 6 US-09-833-381-853 US-09-833-381-853 Sequence BES, Application US/09833381 Fatent No. 6672186 GENERAL INFORMATION: APPLICATIN: Robison, Keith E. TITLE CF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs CURRENT FILING DATE: 2001-04-11 PRIOR FILING DATE: 2001-02-29 NUMBER OF SEQ ID NOS: 2050 SOFTWARE: PastSEQ for Windows Version 3.0 SOFTWARE: PastSEQ for Windows Version 3.0 TYPE: DNA	ORCANISM: ORCANISM: OPGRA33381 ignment Scor ed. No.: ore: rcent Simila st Local Sim ery Match: :		10 110 110 110 110 110 110 110 110 110

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990 TGATAAAAACCCAGAAGAGTCCAAGATCCAAGCAAAACTACCGTGCGATGCCTGGAAGC 1049
750 TGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCT 809
                                                                                                                                                                         930 CAAAGTAGTAAAGGGGGGAGAAGGCCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAAC
                                                                                              810 GCTAGTGCTTGCTCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA
                                                                                                                                               260 sArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluTh
                                                                                                                                                                                                                                              280 rLysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysTh
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CITY: WASHINGTON
STATE: 0C
COUNTRY: USA
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FLING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 05/021,762
FILING DATE: 15-JUL-1996
ATTONINY/AGENT INFORMATION:
WAND: CREEK PATENTINE TO THE TO 
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Matches:
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APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 12, Application US/08892880; Patent No. 5942417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: STEFFE, ERIC K
REGISTRATION UNDRER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-371-2600
TELEFAX: 202-371-2640
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
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US-08-892-880-12
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239.00
99.38%
99.38%
                                                                                                              MOLECULE TYPE: DNA (genomic) FEATURE:
                         LENGTH: 2313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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91..153
     SEQUENCE CHARACTERISTICS
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154..1056
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Best Local Similarity:
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LOCATION:
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FEATURE:
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36,688
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36.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I: 498 base pairs
nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                     US-08-892-880-15
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                                                                                                                                                                                                                                         CTGAATTTCACAGAAGCTAAGGAGGCTGTAAGGTTGCTNGGACTAAGTTTGGCCGGCAAG 311
                                                                                                     132 ACTICCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAGAGACTTTCC 191
                                                                                                                                                                            192 ATCCAGGTGTCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 PheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThr 238
                                                                                                                                         32 IleGlnValSerCysArglleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGln 51
                                                                                                                                                                                                                        71
                                                                      ThrSerIleTrpThrThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSer 31
                                                                                                                                                                                                                    LeuAsnPheThrGluAlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLys
                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08892880

Patent No. 5942417

GENERAL INFORMATION:

APPLICANT: GENTZ, REINER L.

APPLICANT: GINVENTION:

APPLICANT: GINVENTION: CD44-LIKE PROTEIN

INVERS PROVIDENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSIER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

CITY: WASHINGTON

STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

CITY: WASHINGTON

STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

CITY: WASHINGTON

STREET: 1100 NOBER: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE READABLE FORM:

MEDIUM TYPE READABLE FORM:

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTION DATA:

STRING DATE: HERRWATH

FILING DATE: HERRWATH

CLASSIFICATION NUMBER: US/08/892,880
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Mismatches:
Indels:
                                US-10-079-111-1 (1-322) x US-08-892-880-12 (1-492)
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Matches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-UTL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFRENCE/DOCKET NUMBER: 1488.
TELECOMMUNICATION INPORMATION:
TELEPAX: 202-371-2600
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Best Local Similari
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Pred. No.:
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239 AlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyr 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 CTTGGATTTTGCTATGTCAAAGGTATGTNAAGGCCTTCCCTTTTACAAACAAGAATCAG 73
15 TITGITGAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAAGGTGTCCCCACG
                                                                                                   75 GCTCTGCTAGTGCTTTGCTCTTTTTTTTGGTGCTGCTGGTCTTGGATTTTGCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 GlnLysGluMetIleGluThrLysValValLysGluGluLysAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, NW, SUITE 600 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTEND SYSTEM: PC-DOS/MS-DOS
SOFTEND RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HERBWITH
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGRIT INFORMATION:
NAME: STEFFE. RPIC V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/08892880 Patent No. 5942417 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-D
                                                                                                                                                       259 VallysArgTyrVallys 264
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             719 GCAGCATTCAAGAACGAAGCAGCTGGGTTTGGAGGTGTCCCCACCGCCCTGCTGCTGGTGTCT 778
                            | Sequence 28, Application US/09724864
| Sequence 28, Application US/09724864
| Patent No. 6380362
| GENERAL INFORMATION:
| APPLICANT: Watson, James D
| APPLICANT: Watson, James G
| TITLE OF INVENTION: Polymucleotides and methods for their use:
| TITLE OF INVENTION: Polymucleotides and methods for their use:
| TITLE OF INVENTION: Polymucleotides and methods for their use:
| TITLE OF INVENTION: Polymucleotides and methods for their use:
| FILE REPERBNCE: 11000.1050U1
| CURRENT APPLICATION NUMBER: US/09/724,864
| CURRENT FILING DATE: 1999-12-23
| NUMBER OF SEQ ID NOS: 72
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 28
| LENGTH: 1896
| TYPE: DNA | TYPE: DNA | SOFTWARE: Munse | US-09-724-864-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Williams, F. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
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Matches:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Roy, Margaret Ann
Stewart, Timothy A.
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Gerritsen, Mary E.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 10466-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goddard, A.
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-907-794A-205
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RESULT 11
US-09-724-864-28
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT
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) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: oligonucleotide probe
US-09-907-794A-205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00000
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Mismatches:
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Matches:
CURRENT AFPLICATION NUMBER: 2001-07-17
PRIOR APPLICATION NUMBER: DCC/USOO/04414
PRIOR FILING DATE: 2001-02-2
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
PRIOR 
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Filvaroff, Ellen
Fong, Sherman
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ORGANISM: Artificial Sequence
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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US-10-079-111-1 (1-322) x US-09-905-125A-205 (1-50)
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APPLICANT: Sewart. Timochy A.
APPLICANT: Tumas, Daniel
APPLICANT: Mood, William, P. Wickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-144
FILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT FILIAG DATE: 10400-02-22
FILIAG APPLICATION NUMBER: PCT/US00/04414
FRIOR FILIAG DATE: 10409-07-28
FRIOR PRICATION NUMBER: PCT/US09/2054
FRIOR PAPLICATION NUMBER: PCT/US09/20109
FRIOR FILIAG DATE: 1040-07-28
FRIOR APPLICATION NUMBER: PCT/US09/2011
FRIOR FILIAG DATE: 1040-07-28
FRIOR APPLICATION NUMBER: PCT/US09/2011
FRIOR FILIAG DATE: 1040-07-28
FRIOR FILIAG DATE: 1040-07-28
FRIOR APPLICATION NUMBER: PCT/US09/2011
FRIOR FILIAG DATE: 1040-07-28
FRIOR APPLICATION NUMBER: PCT/US09/2011
FRIOR APPLICATION NUMBER: PCT/US09/2009

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Mismatches:
Indels:
Gaps:
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                                                                                                           Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                 Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P.
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
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                                                                                  Goddard, A.
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Query Match:
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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59 GluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnVal
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PRIOR APPLICATION NUMBER: US 60/145,048
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PAPLICATION NUMBER: PCT/US99/28564
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PAPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-02
PRIOR PAPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-06
PRIOR PRING DATE: 1999-12-06
PRIOR DATE: 1999-12-06
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CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
                                                                                                                                                                                                                             ; Sequence 205, Application US/09902775A; Patent No. 6686451
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Grimaldi, Christopher J.
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Mather, Jonnie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Ferrara, Napoleone
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Goddard, A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Gao, Wei-Qiang
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| PRIOR FILING DATE: 1999-12-20
| PRIOR PRICRAPPLICATION NUMBER: PCT/US00/00219
| PRIOR FILING DATE: 2000-01-05
| NUMBER OF SEQ ID NOS: 423
| SEQ ID NO 205
| TYPE: DAA | PRIOR FILING DATE: 2000-01-05
| TYPE: DAA | PRIOR FILING DATE: 2000-01-05
| TYPE: DAA | PRIOR FILING DATE: 2000-01-05
| TYPE: DAA | PRIOR MATION: 01990nucleotide probe | PRIOR INFORMATION: 01990nucleotide probe | PRIOR INFORMATION: 01990nucleotide probe | Proceed. No.: 16.00 | Matches: 16 | Percent Similarity: 100.00$ | Matches: 0 | Percent Similarity: 100.00$ | Masmatches: 0 | Percent Similarity: 100.00$ | Masmatches: 0 | DBs: 4.97$ | Gaps: 0 | DBs: 4.97$ | Pindels: 0 | DBs: 4.97$ | Pindels: 0 | DBs: 0
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Search completed: September 16, 2004, 04:50:06 Job time: 109 secs



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BD172392 Secretced
BD172711 Secreted
BD173149 Secreted
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BD17318 Secretced
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BD07623 Homo sapi
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 200000000
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                               421 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
                                                                               ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
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Hayashi,K.
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Patent: EP 1067182-A 149 10-JAN-2001,
Helix Research Institute (JP)
Location/Qualifiers
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/product = "hyaluronic acid receptor"

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BFIVSDSTYSVASPYSTIPPAPATIPPAPASTSIPRRKKLICVTEVFWETSTWGTETEP
FVENKAARKNBAARGGGGYPTALLIVLALLFFGAAAGLGFCYVKRYVKRPFFTNKNQQKE
MIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCIEBEV"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Winkelmann, J.C., Basu, S., Ozdemir, E. and Blough, R.I.

Direct Submission

Direct Submission

Submitted (11-FEB-1999) Hematology-Oncology, University of Submitted (11-FEB-1999) Avenue, Cincinnati, Ohio 45267-0508,
                                                                                                                                                                                                                                                                                                                                                                                                                 Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, U (2012) (Dasses 1 to 1285) (Dasses 1 to 1285) (Dasses 2 to 1885) (Dasses 2 to 1885)
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  sapiens hyaluronic acid receptor (HAR) mRNA, complete cds
                                                                                                                                                             1 (bases 1 to 1285)
Winkelmann, J. C., Basu, S., Ozdemir, E. and Blough, R. I.
HAR: a novel homolog of CD44 and putative hyaluronic encoded by a gene on human chromosome 11p15
Unpublished
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/mol_type="mRNA"
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/gene="HAR"
121 . 1089
/gene="HAR"
/note="HAR"
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JP 2002017376-A/75
22-JAN-2002
07-UUL-2000 JP 2000253173
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU
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                                            LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
                                                                                                                               261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMet1leGluThr
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                                                                                   921 CTAGTGCTTGCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1755)
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Hayashi,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secretory protein or membrane protein
Patent: JP 2002017376-A 75 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017376-A/75
PD 22-JAN-2002
PP 07-JUL-2000 JP 200253173
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIK
PI KOJI HAYASHI
PC
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/db_xref="cd1:142726"

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Direct Submission
Submitted (20-MR-2002) Takao Isogai, Helix Research Institute,
Submitted (20-MR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 153-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
HRI human DNA sequencing project, CDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing: Helix
Research Institute (supported by Japan Key Technology Center etc.);
cDNA library construction: Institute of Medical Science, University
of Tokyo, Laboratory of Genome Structure, Human Genome Center.
Location/Qualifiers
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Primates; Catarrhini; Hominidae; Homo.
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                                                                                                  Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K., Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T., Makamura,Y., Nagahari,K., Sugano,S. and Isogai,T. HRI human cDNA sequencing project
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Matches:
Conservative:
capping, fis (full insert sequence)
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Indels:
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Isogai, T. and Yamamoto, J.
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                   Homo sapiens (human)
Homo sapiens
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Mammalia; Eutheria;
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                                                                                         41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
                                                                                                                                                          CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
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\(\frac{1}{2}\)	8 8 8 8	3 名 & i	g & g	8 8 8	9	8 8 8 8	8 6 6	Qy Dp	6 B 6	Db RESULT 6 RD22271R	LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
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Sabkenazi, A., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N., Filvaroff, B., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, R., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J. Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I. Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
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                          ProGlullelleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr
                                                                  603 CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACAACAACAACA
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         Ammalia: Eutheria; Primates; Catarrhin; Hominidae; Buffeleosfomn;
Mammalia: Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 2029)
RS Jal, P., Tang Y.T., Gorgone, G.A., Corley, N.C., Guegler, K.J.,
Baughn, M.R., Akerblom, T.B., Young, J.A., Yue, H., Patterson, C.,
Reddy, R., Hillman, J.L. and Bandman, O.
Human signal peptide-containing protein
AL Patent: JD 2002519030-A 64 02-JUL-2002;
INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002519030-A/64
PD 02-JUL-2002
PF 25-JUN-1999 US 60/102686, 11-DEC-1998 US 60/1034983 PR
26-JUN-1999 US 60/102686, 11-DEC-1998 US 60/103129 PI PREETI
LAL, Y TOM TANG, GINA A GORGONE, NBIL C CORLEY, KARL J PI GUEGIER,
PI CHADRA PATTERSON, ROOPA REDDY, JENNIFER I HILLMAN, OLGA BANDMAN
PC CLANDRA PATTERSON, ROOPA REDDY, JENNIFER I HILLMAN, OLGA BANDMAN
PC CLANDRA PATTERSON, ROOPA REDDY, JENNIFER I HILLMAN, OLGA BANDMAN
PC CLANDRA PATTERSON, ROOPA REDDY, JENNIFER I HILLMAN, OLGA BANDMAN
PC A61P25/00, A61P25
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Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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Incyte Clone No: 3044710
Location/Qualifiers
Source 1. -2029
/organism='Homo sapiens (human)'.
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1. 2029
/ Organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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   Eukaryota; Metazoa; Chordata;
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JOURNAL
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                                                                                                AUTHORS
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS		AX092274 Sequence 5 AX092274 AX092274.1	atent 444451	2372 bp WO0116318.	DNA	linear	PAT 21-MAR-200
SOURCE ORGANI	WSI	Homo sapiens (hum Homo sapiens Eukaryota; Metazo Mammalia: Rutheri	ns (human) ns Metazoa, Chor Metazoa, Chor	Chordata; Crani primates: Catar	iata; V	ertebrata; Hominidae	Euteleostomi;
REFERENCE AUTHORS	O1 Fr	Eaton, D.L., Godowski, P.	Filvaroff, E.	., Gerritsen, M.E.	3, M.E.,	Goddard, A Watanabe	
TITLE		Wood,W.I. Secreted ar	nd transmembra	ane polypeptic	cides	and nucleic	acids encoding
JOURNAL FEATURES SOUR	U	Patent: WO Genentech, Ic	Genentech, Inc. (US) Location/Qualifiers  1. 2372	08-MAR-2001, Eiers	.,		
ORIGIN		~ <sup>*</sup> ~	/db_xref="taxon:9"	apiens" gned DNA 606"	=		
Alignment S Pred. No.: Score: Percent Sim Best Local Query Match DB:	nt Scoree 10.: Similari cal Simil	ores: larity: imilarity:	0 322.00 100.00% 100.00% 6	Length: Matches: Conservati Mismatches Indels: Gaps:	: ative: nes:	2372 322 0 0 0	
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ζς Q	16	н о	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 	ValLeuLeuLer 	Thrser	11eTrpThrTh	hrArgleuleu 20 
δ	7	21 ValGlnGly	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArglleMetGly	31uGluLeuSe	rilegin	ValSerCysAr	rgileMetGly 40
ηρ	22	0	TCTTTGCGTGCAC	SAAGAGCTTTC	CATCCAG	GTGTCATGCAG	
& B	41		IleThrLeuValSerLysbysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAl 	AlaAsnGlnGlr	TeuAsn	PheThrGlual	aLysGluAla 60             "Taaggaggg 339
λŏ	9		CysargleuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	LeuAlaGlyLy	AspGln	ValGluThrAl	80
qq	340			TGGCCGGCAAC	GACCAA	GTTGAAACAGO	
상 점	8 04	H 0	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArglle	31yTrpvalgl)	AspGly	Phevalvall1	leSerArgile 100              CTCTAGGATT 459
ò	10	н	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeu1leTrpLysValProVal	ysAsnGlyVa]	[GlyVa]	LeulleTrpLy	ysvalProval 120
qu	46	0	CCCCAAGTGTGGG	AAAAATGGGGT(	GGTGTC	CTGATTTGGA	4GGTTCCAGTG 519
δλ	12	н	SerArgGlnPheAlaAlaTyrCysTyrAsnSerGerAspThrTrpThrAsnSerCys11	CysTyrAsnSe	SerAsp	ThrTrpThrAs	e 14
qq	52	0	STTTGCAGCCTATI	igrracaacre	TCTGAT.	actregacta	Ī 57
<i>장</i> 염	14.	- 0	ProgluileilethrthrtysAspProilePheAsnthrGlnthrAlathrGlnthrthr 	AspProllePhe	PABRITHE SAACACT	GlnThrAlaTh 	rGlnThrThr 160                acaaacaaca 639
<b>상</b> 원	16	н о	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAl. 	ChrTyrSerVa] 	Alaser           GCATCC	ProTyrSerTh	nrileProAla 180 
& g	18	и— о С— Б	roThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIl. 	eroalaserth: 	Serile:	ProargargLy             ccacggagaaa	rsLysLeuile 200              \AAAATTGATT 759

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201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220 	a vo	 160 ATGGCCAGGT 21 ValGlnGlyS
GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240	qq	
cadantadaccaccattcadadaticadacticcticacgitticadagitcicccaccaccaccid 879 Levinilleuhlateuheuhephechyaladladladladladlagityeetstyrvallys 260	y da	41 IleThrLeuVe            280 ATCACCCTTG
880 CTAGIGCTIGCICCTCTTCTTIGGTGCTGCAGCTGGTCTTTGGTTTTTGCTATGTCAAA 939	δ	61 CysArgLeul
261 ArgTyrVallysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280 	a &	340 TGTAGGCTGC 81 SerPheGluT
LysValvallysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	qq	
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	ò	
321 GluVal 322               1120 GAAGTT 1125	දු දු	520 AGCCGACAGT 141 Progluilei
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AX454446 2372 bp DNA linear PAT 06-JUL-2002 Sequence 31 from Patent WO0208284.	δλ	
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	Š A	181 ProThrThrT          700 CCTACTACTA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	δλ	201 CysvalThrG
<pre>Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,</pre>	qa .	
radul, N.F., brepnan, J.F., waranabe, C.K., Williams, P.M., Mood, W.I. and Y.E.W.	ờ i	
Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis	qo ,	
Fatent: WO U208284-A 31 31-UAN-2002; Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,	ර් ප්	241 LeuValLeuA] 
(US) ; GOUGHSKI, FAULU: (US) Kenneth J. (US) ; Marsters, I, Nicholas F. (US) ; Stephan,	ð	
P. Mickey (US)	ය <u>ද</u>	940 AGGTATGTGAA
1. :2372 Arranianianian caninnu	Š	281 LYSVAIVAIL
/organism="nomo sapiens" /mol_type="unassigned DNA" /db xref="taxon:5606"	g ò	1000 AAAGTAGTAAA
	7 음	
Length:	δλ	321 GluVal 322
Matches: Conservative: Wiematcher:	ДC	 1120 GAAGTT 1125
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MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20	VERSION	AX490924.1 C

PAT 16-AUG-2002 1119 219 399 ThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile 100 ProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120 PheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140 ValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180 819 AlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaleu 240 AlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260 ProGluGluSexLysSexProSexLysThrThrValArgCysLeuGluAla 320 GTGAGCAAAAAGGCGAAACCAGCTGAATTTCACAGAAGCTAAGGAGGCC 339 []eThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr 160 200 759 220 280 666 40 9 ValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla ysalaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr SerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly ThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle linear DNA 2372 bp from Patent W00200690. GI:22323799 5

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Indels:
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60/059113,17-SEP-1997 U

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60/06287.17-0CT-1997 U

60/063814,24-0CT-1997 U

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60/063120,24-0CT-1997 U

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                                      Patent: JP 2001516580-A 165 02-OCT-2001;
GENENTECH INC
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1. 2372
Argan="Hono sapiens"
//ncganism="Hono sapiens"
//mol_type="genomic DNA"
/db_xref="taxon:9606"
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US 60/059115,
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                                                                                                              OS Homo sapiens (human)
PN JP 2001516580-A/165
PD 02-OCT-2001
PF 16-SEP-1998 JP 200051
PR 17-SEP-1997 US 60/05912
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Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
                                                                                                                       TGTAGGCTGCTGGGACTTAGGTTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
                                                                                                                                                                                                     SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle
                                                                                                                                                                                                                                         AGCTTTGAAACTTGCGGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT
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                                                                                                                                                                                                                                                                                                                                                                          AGCCCAAACCCCCAAGTGTGGGAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
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BD075532.1 GI:22621135
JP 2001516580-A/165.
Homo sapiens (human)
Homo sapiens
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(C12P21/02,C12R1:645),C12N15/00,C12N5/00
CC Secreted and transmembrane polypeptides and nucleic CC acids
    nucleic acids encoding
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C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21,
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97 US 60/066453, 25-NOV-1997 US 60/066840 PI
WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA,
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60/063127 |
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    .2372
/organism='Homo sapiens (human)'.

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    and transmembrane polypeptides
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Patent: JP 2002223786-A 165 13-AUG-2002;
GENENTECH INC
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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PN JP 2002223786-A/165
PD 13-AUG-2002
PF 18-DEC-2001 JP 2001385135
PR 17-SEP-1997 US 60/059115
17-SEP-1997 US 60/059115
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PR 17-SEP-1997
PR 17-SEP-1997
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PR 28-OCT-1997
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Best Local Similarity:
Query Match:
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ATCACCCTTGTGAGCAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 339
                                                             SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle 100
                                                                                                                                                 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal 120
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2372)
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
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BD172392.1 GI:28413692
JP 2002223786-A/165.
Homo sapiens (human)
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AUTHORS
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C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21,
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(C12N5/00,C12R1:91)
CC Secreted and transmembrane polypeptides and nucleic CC acencoding the same
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60/066840 PI
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organism='Homo sapiens (human)'
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                  Patent: JP 2002238586-A 165 27-AUG-2002;
GENENTECH INC
OS HOMO Sapiens (human)
PD JP 2002238586-A/165
PD 27-AUG-2002
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1. 2372
/ Organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2372)
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.
                                                                        TGTAGGCTGCTGGGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCT
                                                                                                                        SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
                                                                                                                                                AGCTTTGAAACTTGCAGCTATGGCTTGGGTTGGAATGGATTCGTGGTCATCTCTAGGATT
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                                       CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
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JP 2002238586-A/165.
Homo sapiens (human)
Homo sapiens
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 Pennica, D.,
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                        Secreted and transmembrane polypeptides and
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 Gurney, A.L., Goddard, A.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2372)
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                                                                                                                                                                                                                         CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA
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                                                                   AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTTAGGATT
                                                                                                                                                       SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuileTrpLysValProVal
                                                                                                                                                                                AGCCCAAACCCCCAAGTGTGGGAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
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DIANE PENNICA,
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    Gurney, A.L., Goddard, A., Pennica, D., Zheng, J.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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OS Homo sapiens (human)
PN JP 2002238588-A/165
PD 27-AUG-2002
PF 18-DEC-2001 JP 200138
PR 17-SEP-1997 US 60/
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Catarrhini; Hominidae; Homo.
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                               CysArgheuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
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BD173349.1 GI:28414660
JP 2002238588-A/165.
Homo sapiens (human)
Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Cz
Mammalia; Eutheria; Primates; Ca
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C12N1/19,C12N1/21,C12N5/10//A61K38/00,A61K39/395,A61K39/395,
A61P43/00,
C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),(C12N5/10,C12R1:91),
C12R1:91),
C12N15/00,C12N5/00,A61K37/02,(C12N5/00,C12R1:91)
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| CI2N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06,
| A61P25/00,
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Patent: JP 202253280-A 165 10-SEP-2002;
GENENTECH INC
OS Homo sapiens (human)
PN JP 202253280-A/165
PD 10-SEP-2001 JP 2001385319
PF 18-DEC-2001 JP 2001385319
PR 17-SEP-1997 US 66/059115,17-SEP-15
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Conservative:
Mismatches:
Indels:
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60/05926,13-0CT-1997 U

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60/06388,24-0CT-1997 U

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J.
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JP 2002253280-A/165.
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EFIVSDSTYSVASPYSTPAPAPASTSIPTRKKKLICVTEVFWETSTMSTETEP
FVDENKAAFKNEAAGGGGVPTALLVTALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKE
MIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAEV
                       Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lec', J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAQ89284.1"
/db_xref="GI:37182968"
/translation="MARCFSLVLLITSIWTTRLLVQGSLRABELSIQVSCRIMGITLV
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Submitted (01-AUG-2003) Department of
Inc., 1 DNA Way, South San Francisco,
Location/Qualifiers
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//organism="Homo sapiens"
//mol_type="mRNA"
//db xref="taxon:9606"
/clone="DNA34431"
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/locus_tag="UNQ230"
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/note="PRO263"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                         460 AGCCCAAACCCCAAGTGTGGGAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
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GTCCAAGGCTCTTTGCGTGCAGAAGACTTTCCATCCAGGTGTCATGCAGAATTATGGGG
                                                                         IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
                                                                                                         280 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
                                                                                                                                                                                                                                                                                 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
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                                                                                                                                                                                CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
                                                                                                                                                                                                                               340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
                                                                                                                                                                                                                                                                                                                             400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTTAGGATT
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2372 bp mRNA linear PRI 03-0C<sup>3</sup>

Homo sapiens clone DNA34431 XLKD1 (UNQ230) mRNA, complete cds
AX358925

AX358925-1 GI:37182967

FLI CDNA.
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Homo sapiens (human)
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Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Scherch, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Scherch, J.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial nalysis of more than 15,000 full-length human and mouse cDNA sequences  L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  E. 2188257.  E. 2188257.  E. 2188257.  Direct Submission  Strausberg, R.  Direct Submission  Generation (MGG), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USE, MCC Project URL: http://mgc.nci.nih.gov  Contact: MGC help desk  Contact: MGC help desk  Email: cgapbs-r@mail.nih.gov  Contact: MGC help desk  Contact: MGC help desk	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 37 Row: c Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729910.  RES Location/Qualifiers 1. 2282 /organism="Homo sapiens" /Ab_xref="taxon:9606" /clone="MGC:22159 IMAGE:4712863" /tissue type="Liver" /clone_ID="NIH MGC 76" /lab_host="DH10B"		feature Scores:  milarity:
TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL REMARK COMMENT	FEATURES	gene CDS	misc_ ORIGIN Alignment Pred. No.: Score: Percent Si
0y 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120 460 AccCAAACCCAAACCCAAAAAAAAAAAAAAAAAAAAAA	261 ArgTyrValLysAlaPheProPheThrasnLysAsnGlnGlnLysGluMetileGluThr 261 ArgTyrValLysAlaPheProPheThrasnLysAsnGlnGlnLysGluMetileGluThr 362 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGAAGGAAATGATCGAAACC 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 1000 AAGGTAGGAAGGGAAGGCCATGATGATGAGGAATCAAAGAAAACT 301 AgpLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 1060 GATAAAAAACCCAAGAAGATCCAAGGAAACTACGGGATGCCTGGAAGCT 321 GluVAl 1322	RESULT 19 BC026231 LOCUS BC026231 LOCUS BC026231 LOCUS BC026231 BC026231 ACCESSION BC026231 B	Klausner, K.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Vadin, T.B., Tooshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

06-JUL-1999

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receptor LYVE-1

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BFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEP

PVENKAAFKNEARANDSNPNEESKKTDKNDEESKSPSKTTVRCLEAEV"

MIETKVVKEERANDSNPNEESKKTDKNDEESKSPSKTTVRCLEAEV"
                                                                                                                                                                                                                                                                                                                        Jackson, D.G., Banerji, S. and Ni, J.

Direct Submission

Direct Submission

Direct (06-JAN-1999) MRC Human Immunology Unit, Univ. of Oxford, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91. _.1059
/note="CD44-like cell surface hyaluronan receptor; member
of LINK superfamily; HUVEC"
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                                                                                                                                                                         Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                 AFILBIOB
2313 bp mRNA linear PRI 06-JUL-1
Homo sapiens lymphatic endothelium-specific hyaluronan receptor
LIYVE-1 mRNA, complete cds.
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/product="lymphatic endothelium-specific hyaluronan
                                                                                                                                                                                                                    Tammi, R.,
                                                                                                                                                                 Eukaryotza, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Butheria, Primates, Catarrhini, Hominidae,
1 (bases 1 to 2113)
Banerji,S., Ni,J., Wang,S.X., Clasper,S., Su,J., Tamm
and Jackson,D.G.
LYVB-1, a new homologue of the CD44 glycoprotein, is
lymph-specific receptor for hyaluronan
J. Cell Biol. 144 (4), 789-801 (1999)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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183.00
98.15%
98.15%
56.83%
                                                                                                                                         Homo sapiens (human)
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 Mismatches:
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Mammalia; Butheria; Primates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 716)
Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
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JP 2002017376-A/278
22-JAN-2002
07-JUL-2000 JP 2000253173
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU
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C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
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Secretory protein or membrane protein
FH Key Location/Qualifiers
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Patent: JP 2002017376-A 278 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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JP 2002017376-A/278.
Homo sapiens (human)
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                aSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIl
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Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Bayashi,K.
Secretory protein or membrane protein
Patent: EP 1067182-A 451 10-JAN-2001;
Helix Research Institute (JP)
Location/Qualifiers
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PAT 18-SEP-2002

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SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArg11e 100
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misc_feature 289..453
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misc_feature 222..289
sig_peptide 104..151.
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id AA046671
   region 1. .133
id AA081350
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identity 90
region 269.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (basea I to 451)

Edwards, J. B.D.M., Duclert, A. and Lacroix, B.

5' EST of tissue-nonspecific secretory protein

GENSET
OS Homo sapiens (human)

N JP 201512011-A/94

PD 21-AUG-2001

PP 31-JUL-1998 JP 2000505289

PR 01-AUG-1997 US 08/905135
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            sapiens (human)'.
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BD076146
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Matches:
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Mismatches:
Indels:
           /organism='Homo sa
Location/Qualifiers
1. 716
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Homo sapiens (human)
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AUTHORS
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complement(1669. .1967)
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7758. .3314
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13011. 13042
/rpt_family="polypurine"
complement(13275. 13367)
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18394. .18518
'rpt f-.'
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[ement(17735)
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complement(17287. .17414)
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9831. .9885
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complement(8705. .8773)
/rpt_family="Charlie8"
complement(8833. .9094)
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complement(17438._.
  Location/Qualifiers
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1938. .11983
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8859. .19091
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    FEATURES
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Submitted (165-840G-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

18 3 (bases 1 to 165698)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chazoro, B., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ginde, S., Goyette, M., Graham, L., Grand Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamata, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Mehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marthews, C., Macdonald, P., Major, J., Marthews, C., Macdonald, P., Major, J., Marthews, C., Macdonald, P., Major, J., Marthey, T., Naylor, J., Nguyen, C., Orman, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nail, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Santos, R., Schauer, S., Schupback, R., Seman, J., Spencer, P., Stense, M., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, K., Vo, A., Wilson, B., Wu, X., Wayman, D., Ye, W.J., Young, G., Lainer, S., Subplission, Direct, Subhission
                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Deyare, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Mardis, J., Molla, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M., Nagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M., Nagner, A., Direct Submission
                                                   PRI 07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (07-SEP-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 7, 2001 this sequence version replaced gi:14627146. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                               Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165698)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                ACO09532 165698 bp DNA linear PRI 07-SEI
HOmo sapiens chromosome , clone RP11-58H20, complete sequence.
ACO09532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project_Information
                                                                                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome, clone RP11-58H20 Unpublished
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Center clone name: 58_H_20
                                                                                                                      AC009532.9 GI:15487414
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                                                                                                                                                                  Homo sapiens (human)
                                                                  DEFINITION
                                                                                                                                                                SOURCE
ORGANISM
RESULT 24
AC009532/c
                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
JOURNAL
REFERENCE
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12247 ATTCCACGGAGAAAAAAATTGATTTGTGTCACAGAAGTTTTTATGGAAACTAGCACCATG 12188
                                                                                                                                                                                                                                                                                                             BD077623 363 bp DNA linear PAT 27-AUG-2002 5'EST of secreted protein expressed in muscles and other mesodermal tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 363)
Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
5'EST of secreted protein expressed in muscles and other mesodermal tissues
                                                                                                                                                                 SerThrGluThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGly 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C12N15/09, C12N15/09, C07K14/47, C12M1/00, C12N15/00, C12N15/00 CC
                                                                 12307 TCCCCTTACTCTACAATACCTGCCCCTACTACTACTCCTCCTCCTGCTCCAGCTTCCT
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                                                                                                         193 IleProArgArgLysLysLeuIleCysValThrGluValPheMetGluThrSerThrMet
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JP 2001512016-A/209
21-AUG-2001
31-JUL-1999 JP 2000505295
01-AUG-1997 US 08/905134
JEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLERT, BRUNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent: JP 2001512016-A 209 21-AUG-2001;
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Location/Qualifiers
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n=a, g, c or t
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JP 2001512016-A/209.
Homo sapiens (human)
Homo sapiens
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id AA046671
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Matches:
Conservative:
Mismatches:
Indels:
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complement(22064...2151)
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complement(22164...22466)
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complement (36989. .37096)
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complement (37280, .37341)
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37951, 37997
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family="(TA)n"
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_family="MIR"
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family="MIR"
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complement (39968.
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family="L2"
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3458. .33462
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FEATURES

ORIGIN

(1-165698)

x AC009532

US-10-079-111-1 (1-322)

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153 ThrGlnThrAlaThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAla 172

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US-10-079-111-1 (1-322) x BD073800 (1-373)
                                                                                                                                                                                       Bos taurus (cow)
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Pred. No.:
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TITLE
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JP 2001512012-A/204
21-AUG-2001
31-AUG-1997 US 08/905279
DUMAS MILNE EDWARDS JEAN BAPUTIST, DUCLAIR EIMERIC, LACROIX PI
                                                                                                       C12N15/09,A61K38/00,A61K48/00,C07K14/435,C07K19/00,C12P21/02,C12Q1/68,G01N33/50,G01N33/53,G01N33/53,G01N33/56,C12N15/00,A61K37/02 Strandedness: Double;
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 373)
Baputist, D.M.E.J., Eimeric, D. and Bruno, L. F. Est of secreted protein expressing in testis and other tissues GENSET
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Location/Qualifiers
Location/Qualifiers
1. 373m="Homo sapiens"
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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Matches:
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                                                                                    US-10-079-111-1 (1-322) x BD077623 (1-363)
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                                                                                                                                                                                                                                          BD073800.1 GI:22619403
JP 2001512012-A/204.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Topology: Linear;
identity 98
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id AA081350
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AUTHORS
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| Jaccell. id="MAKFRIGLIASIWTTRILVQGSLRSEEISILGPCRIMGVTLV
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MIETKVVKEEKADDSNPNEESKKMNKTPEEPKSPPKTTVRCLEAEV"
                                                                                                                                                                                                                             MAM 27-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Butleria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. I boses I to 1613)
Huang, S.S., Tang, F.M., Huang, Y.H., Liu, I.H., Hsu, S.C., Chen, S.T. and Huang, J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 CysTyrVallysArgTyrVallysAlaPheProPheThrAsnLysAsnGlnGlnLysGlu 276
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                                            259
                                                                                                                                                                                                                           AX372937 1613 bp mRNA linear MAM 27-OCT-200
Bos taurus cell surface retention sequence binding protein-1 mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22-AUG-2003) Biochemistry & Molecular Biology, St. Loui
University School of Medicine, 1402 S. Grand Blvd., St. Louis, MO
63104, USA
1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning, expression, characterization and role in autocrine cell growth of cell surface retention sequence binding protein-1 J. Biol. Chem. 278 (44), 43855-43869 (2003)
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Indels:
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Matches:
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1. 1613
/organism="Bos taurus"
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Huang, S.S. and Huang, J.S.
Direct Submission
                                                                                                                                                                                                                                                                            complete cds.
AY372937
AY372937.1 GI:36304137
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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mawmaalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (bases 1 to 2027)

Strausberg, K.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altechul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Mooree, T., Max, S. I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Walzh, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bukkesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodrigues, S.J., and Marra, M.A., Generaticald, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Goneration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                         BC038653 2027 bp mRNA linear ROD 07-OCT-2003 Mus musculus extra cellular link domain-containing 1, mRNA (cDNA clone MGC:48237 IMAGE:2936961), complete cds.
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Series: IRAK Plate: 83 Row: m Column: 14
                                                                                                                                                                            Direct Submission
Submitted (15-OCT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-ramal. nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadanosystemshology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                 Conservative:
Mismatches:
                                                                 Indels:
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                                                                                        Gaps:
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Mus musculus (house mouse)
Mus musculus
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                                                                                                                                   US-10-079-111-1 (1-322)
                                   Best Local Similarity:
            Percent Similarity:
                                                          Query Match:
DB:
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BC038653
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KEYWORDS
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                                                       ROD 01-JUN-2001
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LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific receptor for hyaluronan
Jymph-specific receptor for hyaluronan
99156989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / LTAIBILATION="MIQHTSIVFFIASIWTTRHPVQGADLVQDLSISTCRIMGVALVG
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GAAFKNEAAGFGGVPTALLVLALLFFGAAAVLAVCYVKRYVKAFFFTTKNQQKEMIET
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prevo,R., Banerji,S., Ferguson,D.J., Clasper,S. and Jackson,D.G.
Mouse LYVE-1 is an endocytic receptor for hyaluronan in lymphatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="lymphatic endothelial hyaluronan receptor for
hyaluronan uptake"
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                                             MMU311501 1516 bp mRNA linear ROD 01-JUN-
Mus musculus mRNA for lymphatic endothelial hyaluronan receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (16-FEB-2001) Jackson D.G., Institute of Molecular
Medicine, MRC Human Immunology Unit, John Radcliffe Hospital,
Headington, Oxford, OX3 9DS, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVVKBEKADDVNANEESKKTIKNPEEAKSPPKTTVRCLEAEV"
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Matches:
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hyaluronan receptor; LYVE-1 gene.
Mus musculus (house mouse)
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                                                                                           LYVE-1 gene)
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ORGANISM
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abrameson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richtards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu.X., Glbbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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GAARKNEAAGFGGYPTLIVILALIFFGAAAVLAVCYVKRYYKAFPFTTKNQQKEMIET
KVVKEEKADDVNANBESKKTIKNPEEAKSPPKTTVRCLEAEV"
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Location/Qualifiers
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Submitted (25-007-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Producement: Marcello Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadans@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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gene="Xlkd1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 2027)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12477932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 2027)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNKNPOMNFTEANEACKMLGLTLASRDQVESAOKSGFETCSYGWVGEOFSVIPRIFSN
PRCGKNGKGVLIWNAPSSQKFKAYCHNSSDTWVNSCIPEIVTTFYPVLDTQTPATEFS
VSSSAYLASSPDSTTPVSATTRAPPLTSMARKTKKICITEVYTEPITMATETEAFVAS
GAAFKNEAAGFGGVPTALLVLALLFFGAAAVLAVCYVKRYVKAFPFTTKNQQKEMIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MLQHTSLVLLLASIWTTRHPVQGADLVQDLSISTCRIMGVALVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 AlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeuLeuValLeu 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                    This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="extra cellular link domain-containing 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306. .578
/note="LINK; Region: Link (Hyaluronan-binding)"
/db_xref="CDD:smart00445"
                                                                                                                                                                                                                                                                                                         tissue type="Lung, 2 pooled mouse tumors."
clone lib="NCI CGAP_Lu33"
lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVVKEEKADDVNANEESKKTIKNPEEAKSPPKTTVRCLEAEV"
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Matches:
Conservative:
                                                                                                                                                                                            /mol_type="mRNA"
/errain="CZECH II"
/db_xref="taxon:1090"
/clone="MGC:48237 IMAGE:2936961"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAH38653.1"
/db_xref="G1:24047315"
/db_xref="LocusID:114332"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="synonym: Lyve-1"
/db_xref="LocusID:114332"
/db_xref="MGI:2136348"
                                                                                                                                                                                                                                                                                                                                                                                           'note="Vector: pT7T3-Pac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 AlaLeuLeuPhePheGlyAlaAlaAla 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTCTCCTCTTTGGTGCTGCCGCT 935
                                                                                                                                                                 'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-079-111-1 (1-322) x BC038653 (1-2027)
                                                                                                               Location/Qualifiers
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BC038892.1 GI:24416482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="Xlkd1"
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29.00
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                                                                                     analysis.
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DB:
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SOURCE
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Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gabregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Guntatte, P., Haaland, W., Hamilton, C., Hamilton, K., Havlak, P., Hawes, A., Henderson, N., Hernandez, M., Havlak, P., Hawes, A., Henderson, N., Hernandez, M., Havlak, P., Hawel, J., Glebird, D., Jackson, A., Jacob, L., Jiacob, L., Jiacob, E., Hulyk, S., Hung, J., Johnson, R., Liu, Y., Liu, W., Liu, Y., Lebow, H., Levan, J., Lewis, L., Li, L., Lebow, H., Logado, R., Maris, L., Li, Z., Liu, J., Lorado, R., Martin, R., Ma, J., Mahleshwari, M., Mahindarten, M., Mahnoud, M., Martin, S., Manches, J., Mandarten, M., Martin, R., Ma, J., Mandeshwari, M., Mahindarten, M., Martin, R., Ma, J., Mandeshwari, M., Martin, R., Mandeshwari, M., Morris, K., Morris, R., Perez, L., Ffannkoch, C., Okwoon, G., Olarnpunsagoon, A., Pals, S., Paul, H., Perez, A., Perez, L., Ffannkoch, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., J., Raylor, P., Savery, G., Scherer, S., Scorl, G., Shatsman, S., Shen, H., Sheetty, J., Shartspeyn, A., Savery, G., Scherer, S., Scorl, G., Shatsman, S., Shen, H., Sheetty, J., Shors, R., Williams, M., Strong, R., Sutton, A., Svaer, G., Wang, S., Wartspeyn, R., Williams, G., Willsana, D., Waldron, L., Walker, B., Waldron, Y., Wangh, R., Waldron, R., Waldron, Y., Wan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dispect submission.

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23119636.

The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/tarl/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
Direct Submission
Submitted (GB-ANG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235382)
Rat Genome 1 equencing Consortium.
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Consensus quality: 214760 bases at least Q40
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Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: GJNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: CH230-226A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---- Summary Statistics
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Unpublished
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TITLE
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JOURNAL
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Windows, Metzker, Abramzon, S., Adams, C., Alder, J.,
Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Albbrooks, S., Admin, A., Angulano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E. Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, M., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, T., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Davila, M.L., Davis, C., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Durn, A., Durbin, X., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235382 bp DNA linear HTG 13-MAY-2003 ***, 2 unordered pieces. AC130104
                                                                                                                                                                                                                                                                                        849 GCAGCATTCAAGAACGAAGCAGCTGGGTTTGGAAGGTGTCCCCACCGCCCTGCTGGTGCTG 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 ArgTyrVallysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                           224 AlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeuLeuValLeu
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
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                            Percent Similarity:
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Continuation [4 of 4)
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AC110451_1
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AC110451 3/c
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AC130104/c
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Rattus norvegicus clone CH230-39GB, WORKING DRAFT SEQUENCE, 2
unordered pieces.
                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 ArgTyrVallysAlaPheProPheThrAsnLysAsnGlnGlnJysGluMetIleGluThr 280
Consensus quality: 218876 bases at least Q30 Consensus quality: 220968 bases at least Q30 Estimated insert size: 228779; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                           1 231555 contig of 231554 bp in length 231555 231654; gap of unknown length 231655 235382; contig of 3728 bp in length. Location/Qualifiers
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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Mismatches:
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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/note="wgs_end_extension
clone_end:T7"
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/note="wgs_end_extension
clone_end:Sp6"
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clone_end:T7"
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/note="clone_boundary
clone_end:Sp6
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224\overline{2}71. .225117
/note="clone_boundary
clone_end:T7
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226902. .228625
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Manaryote a Merazoa: Choodata; Cranidasa; Varebraha; Buselesoromi; Markaryote a Metria; Rodentia; Solutognathi; Muridae; Murinae; Matteria; Rodentia; Solutognathi; Muridae; Murinae; I that it the control of the contr
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Indels:
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/db_xref="GI:32141034"
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                                                                                                                                                                                                                                                                                                                                                                    organism="Sus scrofa"
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/db_xref="taxon:9823"
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                                                                                                                         Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center: Cade: BCI
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: ngsc-help@bcm.tmc.edu
Center project name: KBXX
Center project name: KBXX
Center clone name: CH230-19G8
Center clone name: CH230-19G8
Assembly program: Phrap; version 0.990329
Consensus quality: 217229 bases at least Q40
Consensus quality: 220365 bases at least Q30
Consensus quality: 220366 bases at least Q30
Consensus quality: 220366 bases at least Q20
Consensus quality: 220366 bases; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is
         and separated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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47066 47165: gap of unknown length
47166 239307: contig of 192142 bp in length.
Location/Qualifiers
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Matches:
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/db_xref="taxon:10116"
/clone="CH230-39G8"
47166. .48705
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59788. .60787
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EAYCHNSSDTRINSCIPEIIPTNDPTFNTNTAPYTTEMTVNRTSSSSTNGPSSSVWP
TVVTTSLPLATTSTPRKRKLICITEAFMETSTISTETELYIENRTAFKNEAIGFGGIP
TALLVLALLFFAAAAGLAVCYVKRYVKAFPFTNKNQQKEMI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAT 18-DEC-2003
Sus scrofa (pig)
Sus scrofa
Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Suidae; Sus.
1 (bases 1 to 603)
Michael, K.W., Xu, S.-H., Voisine, P., Khan, T.A., Feng, J., Li, J.,
Sellke, F.W. and Bianchi, C.
Identification of pig LYVE-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 CysTyryallysArgTyrVallysAlaPheProPheThrAsnLysAsnGlnGlnLysGlu 276
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2 (bases 1 to 603)

Michael,K.W., Xu,S.-H., Voisine,P., Khan,T.A., Feng,J., Li,J.,
Sellke,F.W. and Blanchi,C.

Direct Submission
Submitted (23-MAY-2003) Cardiothoracic Division, Beth Israel
Deaconess Med. Ctr., 330 Brookline Avenue DA-803, Boston, MA 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="lymphatic endothelial hyaluronan receptor
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AR410765
AR410765.1 GI:40162265
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GENBRIFCH INC

DE ATTÍFICIAI SEQUENCE

PN JP 2001516580-A/169

PD 2001516580-A/169

PD 2001516580-A/169

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PD 2001516580-A/169

PR 17-SEP-1997 US 60/059119, 17-SEP-1997 US 60/059117 PR

17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/062319, 17-SEP-1997 US 60/052815 PR

17-CCT-1997 US 60/063486, 24-CCT-1997 US 60/062125 PR

24-CCT-1997 US 60/063146, 24-CCT-1997 US 60/06312 PR

24-CCT-1997 US 60/063146, 24-CCT-1997 US 60/06312 PR

24-CCT-1997 US 60/063145, 24-CCT-1997 US 60/06312 PR

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21-NOV-1997 US 60/064248, 07-NOV-1997 US 60/06419 PR

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21-NOV-1997 US 60/06634, 24-NOV-1997 US 60/06413 PR

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21-NOV-1997 US 60/066410, 24-NOV-1997 US 60/066419 PR

21-NOV-1997 US 60/066466, 24-NOV-1997 US 60/066419 PR

21-NOV-1997 US 60/066466, 24-NOV-1997 US 60/066419 PR

21-NOV-1997 US 60/066466, 
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Secretory and transmembrane polypeptide and nucleic acid encoding
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Description of Artificial Sequence: Synthetic FH
Location/Qualifiers
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                                                          Patent: JP 2001516580-A 169 02-OCT-2001;
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    50
    /organism="synthetic col/mol_type="genomic DNA"
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                                                                                         GENENTECH INC
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VERSION
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BD172396
                                                             JOURNAL
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      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthetic construct
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 50)
Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.
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Secretory and transmembrane polypeptide and nucleic acid encoding
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/mol type="unassigned DNA"
/db xref="taxon:32630"
/nofe="Synthetic Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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Gaps:
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Sequence 205 from Patent WO0104311.
      /organism="unknown"
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Location/Qualifiers
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Best Local Similarity:
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AUTHORS
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BD075536
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Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
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PC C12N5/10,C12R1:91),C12N15/00,C12N5/00,(C12N5/00,C12N5/10,C12R1:91) CC Description of Artificial Sequence: Synthetic FH Key
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the same
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1 (bases 1 to 50)
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
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                                                                                                                      74
                                                                                                                                            GAGGCCTGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTT
                                                                                                                    GluhlacysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnVal
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60/059113,17-SEP-1997 US
60/059113,17-SEP-1997 US
60/059113,17-SEP-1997 US
60/05926,15-0CT-1997 US
60/05281,17-0CT-1997 US
60/05281,24-0CT-1997 US
60/053120,24-0CT-1997 US
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60/066772,24-NOV-1997 US
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18-DEC-2001 JP 2001385248
17-SEP-1997 US 60/059115,17-SEP-1997
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GENENTECH INC
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PN JP 2002238587-A/169
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Best Local Similarity:
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PI JEAN YUAN
PC C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06, PC
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Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
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60/059121 PR
60/059263 PR
60/062125 PR
60/062181 PR
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60/063343 PR
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60/066511 PR
60/066840 PI
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                                                                                                                                                                                                                                                                                                                                                                                                              GAGGCCTGTAGGCTGCTGGGACTAAGTTTTGGCCGGCAAGGACCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                    GluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnVal
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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JP 2002253280-A/169
10-SEP-2002
18-DEC-2001 US 60/059115
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synthetic construct
artificial sequences.
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GENENTECH INC
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PN JP 20022
PD 10-SEP-2
PF 18-DEC-2
PR 17-SEP-1997 U
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Best Local Similarity:
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BD175387
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VERSION
KEYWORDS
SOURCE
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                    FEATURES
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Bukaryota; Fungi Communia Basidiomycota; Hymenomycetes; Homobasidiomycetes; Agaricales; Schizophyllaceae; Schizophyllum.

1 (bases 460 to 5883)

1 (bases 460 to 5883)

Laddiand, J. Vaillancourt, L.J., Hegner, J., Lengeler, K.B.,
Laddison, K.J., Specht, C.A., Raper, C.A. and Kothe, E.

The mating-type locus B alpha 1 of Schizophyllum commune contains a pheromone receptor gene and putative pheromone genes

BMBO J. 14 (21), 5271-5278 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLN 25-0CT-1996
PC A61P25/16,A61P25/28,A61P31/12,A61P35/00,C07K14/47,C07K16/18,
PC C07K19/00,
PC C12N1/19,C12N1/21,C12N5/10//A61K38/00,A61K39/395,A61K39/395,
PC C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),(C12N5/10,PC C12R1:91),
PC C12R1:91),
PC C12N1/00,C12N5/00,A61K37/02,(C12N5/00,C12R1:91) CC Description of Artificial Sequence: Synthetic FH Key Location/Qualifiers 1.50
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Submitted (16-APR-1996) J. Wendland, Philipps-Universitaet Marburg,
Karl-von-Frisch Strasse, 35032 Marburg, FRG
On Apr 17, 1996 this sequence version replaced gi:1246904.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-MAR-1994) J. Wendland, Philipps-Universitaet Marburg, Rall-von-Frisch Strasse, 35032 Marburg, FRG revised by author 05-JUL-95 & 20-SEP-95. Revised by (4) (bases 1 to 5883)
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B alpha pheromone; B alpha pheromone-receptor; bapl gene; barl
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Location/Qualifiers
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/clone="Btr 2-2"
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807 GCGCCTACTACCACTCCGCCTGCACCGGCATCTACG 772
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                                                                                                Search completed: September 16, 2004, 04:01:33 Job time : 4969 secs
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2324. .2390,2443. .2555,2608. .>2819))
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-833-381-849
US-09-907-794A-200
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US-09-902-125A-200
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1201 CTTACCCTGCCCCGGCTGGGGAAATCAAAGGGCCCAAAGAACCCAAAGAAGAAGAAGTCCACC 1260	1321 1328 1381	1388 CACGGCCTTTCTAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGACTTTTGC 1447 1441 AAAGTGCAAGGACCTAAAACATCCTACAGTGGTAAAAGGCCTCCTGGCTGT 1500 1448 AAAGTGCAAGGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGT 1500 1448 AAAGTGCAAGGACCTAAAAACATCTCATCAGTATCCAGTGGTAAAAAAGGCCTCCTGGCTGT 1507	1501 CTGAGGCTAGGTGGATGAAAGCCAAGGACTCACTGAGACCAAGGCTTTCTCTACTGATT 156	1621	1681 GATTCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGCT 1740 	1741	1801	1861 1868	1921 CITAIDAATTICTATTITTAICTGAGTTACAGAATGATTACTAAGGAA 1928 CITAIDAATTICTATTITTATCTAGGTTACAGAATGATTACTAAGGAA	1988 AATTIGTITAAAAAGTAATAAAATCAACAAAAAAAA 2025 1988 AATTIGTITAAAAAGTAATAAATTCAACAACATTIGCIGAATA 2032	SULT 3 -09-833-381-853 Sequence 853, Application US/09833381	FACENIE NO. 887.1008 GENERAL INFORMATION: APPLICANT: Robison, Keith E. TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs	TALE REFERENCE: S800-119 CURRENT APPLICATION NUMBER: US/09/833,381 CURRENT FILING DATE: 2001-04-11 PRIOR APPLICATION NUMBER: 09/516,448	FALOR FILING JAILS: 2000-02-29; NUMBER OF SEQ ID NOS: 2050; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 853; LENGTH: 2404
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                                                    Score 1994; DB
Pred. No. 0;
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99.8%;
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APPLICANT: Gurmada, Christopher J.
APPLICANT: Gurmada, Christopher J.
APPLICANT: Gurmada, Christopher J.
APPLICANT: Rail and Macher, Jennie P.
APPLICANT: Ray, Machae P.
APPLICANT: Pan, Jame B.
APPLICANT: Ray, Michas F.
APPLICANT: Roy, Magaret Ann
APPLICANT: Roy, Magaret Ann
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANTON NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR RELING DATE: 1999-09-13
PRIOR RELING DATE: 1999-09-13
PRIOR RELING DATE: 1999-09-14
PRIOR RELING DATE: 1999-09-15
PRIOR RELING DATE: 1999-09-19
PRIOR RELING DATE: 1999-09-
US-09-907-794A-200

Sequence 200, Application US/09907794A

Sequence 200, Application US/09907794A

GENERAL INFORMATION:
APPLICANT: Genetech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bestein, David
APPLICANT: Besnoyers, Luc.
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                         Godowski, Paul J.
Grimaldi, Christopher
                                                                                                                                                                                              Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
Goddard, A.
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ORGANISM: Homo sapiens
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Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentecth, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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RESULT 5 US-09-905-125A-200 ; Sequence 200, Application US/09905125A

APPLICANT: Askinenzi, Morid
APPLICANT: Askinenzi, Morid
APPLICANT: Benonyers, Luc
APPLICANT: Benonyers, Luc
APPLICANT: Benonyers, Luc
APPLICANT: Benonyers, Luc
APPLICANT: Perzura, Moridene
APPLICANT: Perzura, Moridene
APPLICANT: Foldy Sheman
APPLICANT: Godowski, Paul J.
APPLICANT: Milliami, P. Mickey
APPLICANT: Mulliami, P. Mickey
APPLICANT: Milliami, P. Mickey
APPLICANT: Mulliami, D. Mickey
APPLICANT: Milliami, D. Millia

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Section Similarity  1 ACCOMMENDATION TO THE SECTION OF THE SECTION		y 1104 AAGAGTCCAAGCAAACTACCGTGCGTGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1163	y 1164 TGAGGAGACACACTGAGGCTGGTTTCTTTCATGCTCCTTACCCTGCCCGGCGGAA 1223	1224	Y 1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGCCCTTCTCTTATTGTAAC 1343	Y 1344 CCTGTCTGGATCCTACTCCTACCTCCAAAGCTTCCCACGCCCTTTCTAGCCTGGCTAT 1403	y 1404 GTCCTAATAATATCCCACTGGGAGAAAGGGTTTTGCAAAGGACCTAAAACATC 1463 	y 1464 TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC 1523  1441 TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGTGGGTTGAAAGC 1500	y 1524 CAAGGAGTCACTGAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA 1583	y 1584 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1643 	y 1644 AGAATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1703 	1704	y 1764 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT 1823	1824 CACTGITIAGAACACACACTTACITITICIGGICICIACCACIGCIGATATITICIC 1883	V 1884 AGGADATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTTATCT 1943 	y 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTTAAAAAGTAATAAA 2003 	y 2004 TTCAACAAACATTTAAAAAA 2025 	RESULT 6 US-09-902-775A-200 ; Sequence 200, Application US/09902775A ; Patent No. 6686451 ; GENERAL INFORMATION:
99.34; Score 1994; DB 4; Length 2172; Local Stinlarity 99.34; Pred, No. 0, Local Stin	<b>q</b> a	ਨੇ ਰੀ 	4a -	λο dd ———————————————————————————————————	40 	-	<i>አ</i> ብ	λ <sub>0</sub> α <sub>0</sub>	रु व	<i>ই</i> প্র	λ <sub>o</sub> a	රු <u>සි</u>	<i>ò</i> € € € € € € € € € € € € € € € € € € €	<i>≿</i> 48	<i>ठ</i> व	· 중 옵	<i>₹</i> 40	RES
	ry Match 98.3%; Score 1994; DB 4; Length 2372; E. Local Similarity 99.8%; Pred. No. 0; Ches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps	AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTG	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGGTGCTTCAGCCTG	GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCACGAGGCTCTTTGCGTGCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA	GAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAG	GCGAACCAGCAGCAGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGGGGCTGAAGT 	TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCT	GGCTGGGTTGGACATGGATTCGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGG 	AAAAATGGGGTGGGGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	TGTTACAACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATTATCACCAAA 	GATCCGATATTCAACACTCAAACTGCAACACAAACAACAGAATTTATTGTCAGTGACAGT 	4 ACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCCTACTACTACTACTACTCCTGCT 1 ACCTACTACTACTACTACTCTTACTCTACTACTACTACTA	4 CCAGCTTCCACCTTCTATTCCACGAGAAAAAATTGATTTGTGTCACAGAAGTTTTATG	4 GAAACTAGCACCATGTCTACAGAAACTGAACCATTGTTGAAAATAAAGCAGCATTCAAG	4 AAIGAAGCIGCIGGGITIGGAGGIGICCCCACGGCTCIGCIAGTIGCTCCTCTTC	TTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT	4 TTTACRAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAGGAGGAGGAGAGGAGGAGGAGGAGGAGGAG

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APPLICANT: WOOD, William, I.
TITLE OF INVENTION: Secreted and Transmembrane FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-18
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PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-11-20
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Pred. No. 0;
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Grimaldi, Christopher J.
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Wood, William, I.
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Tumas, Daniel
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Filvaroff, Ellen
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Goddard, A.
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Roy, Margaret Ann
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Hillan, Kenneth,
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Mather, Jennie P.
Pan, James
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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CORGANISM: Homo sapiens
US-09-902-775A-200
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                                                                                                                                 AAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA
                                                                                                              ATCAAAAGGGCCAAAGAACCAAAGAAGAAGTCCACCTTGGTTCCTAACTGGAATCAGC
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                                                        TGAGGAGACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA
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Sequence 1, Application US/08892880 Patent No. 5942417 GENERAL INFORMATION: APPLICANT: NI, JIAN APPLICANT: GENTZ, REINER L.

US-08-892-880-1

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                                                                                                                                                                                                                                                    SOFTWARE PATENTIAL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-7UL-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEPPE, ERIC K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.4%; Score 1915.2;
99.6%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,689
REFERENCE/DOCKET NUMBER: 1488.0490001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                              COUNTRY: USA
ZIF: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 2313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 99.6
Matches 1920; Conservative
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LOCATION:
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LOCATION:
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US-08-892-880-1
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P.L.L.C.

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                                                                                                                                                                                                                 Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                   1488.0490001
                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Bur PC Compatible
COMPARE: Patentin Release #1.0, Ver
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-UUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 12, Application US/08892880; Patent No. 594247; GENERAL INFORMATION:
APPLICANT: NI, JIAN APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 1486
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.5
Best Local Similarity 98.5
Matches 334; Conservative
                                                                                                                         ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                             CORRESPONDENCE ADDRESS:
                                                                CITY: "...
STAIR: DC
COUNTRY: USA
"P: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear ; MOLECULE TYPE: CDNA US-08-892-880-11
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762
                                                     TCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAG 402
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US-08-892-880-11/C
; Sequence 11, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GEN'Z, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
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1578 TCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAG 1637
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TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REPERENCE: 210.121.470C3
CURRENT APPLICATION NUMBER: US/09/389,681A
CURRENT APPLICATION NUMBER: US/09/389,681A
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FASISEQ for Windows Version 3.0
SEQ ID NO 324
LENGTH: 241
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US-09-620-405B-324/C
; Sequence 324, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Uning, Yugiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Hapler, William T.
; APPLICANT: Hapler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILLIG DATE: 2000-07-20
; NUMBER OF SEC ID NOS: 495
; SEC ID NOS: 495
; SEC ID NO 324
; TENNICH C. 244
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11.8%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.7e-60;
Matches 239; Conservative 0; Mismatches 0; Indels
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11.8%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.7e-60;
Matches 239; Conservative 0; Mismatches 0; Indels
APPLICANT: Mitcham, Jennifer L.
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; ORGANISM: Homo sapiens
US-09-389-681-324
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14.6%; Score 296.8; DB 2; Length 492;
Best Local Similarity 98.3%; Pred. No. 2.6e-77;
Matches 298; Conservative 0; Mismatches 5; Indels 0
                       NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
                                                                                                                                                                         COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0490001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371_-2600
     CD44-LIKE PROTEIN
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; Sequence 324, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: HEREMITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 492 base pairs TYPE: mucleic acid strandeDNESS: single
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11.8%; Score 239; DB 4; 1 100.0%; Pred. No. 1.7e-60; tive 0; Mismatches 0;

Length 241;

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1578 TCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAG 1637
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                                                                                                              Query Match
Best Local Similarity 100.(
Matches 239; Conservative
                    ; ORGANISM: Homo sapiens
US-09-604-287A-324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-834-759-324/c
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GENERAL INFORMATION:

APPLICANT: Jiang, Yuqui
APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Xu, Jiangchun
APPLICANT: Jiangc
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GENERAL INFORMATION:
APPLICANT: Jang, Yuqiu
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER; CURRENT APPLICATION NUMBER: 2000-06-22
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FaetSEQ for Windows Version 3.0
LENGTH: 241
TYPE: DNA
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100.0%; Pred. No. 1.7e-60;
Live 0; Mismatches 0;
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US-09-433-826B-324
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APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Miccham, Jannifer L.
APPLICANT: Ku, Jiangchun
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, Discours Susan b.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REPERENCE: 210121.470C9
CURRENT APPLICATION NUMBER: US/09/834,759
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NUMBER OF SEQ ID NOS: 547
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                     ; Sequence 324, Application US/09834759
; Patent No. 6680197
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Best Local Similarity 100.
Matches 239; Conservative
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ORGANISM: Homo sapiens
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Post-processing: Listing first 100 summaries

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AAB88419. Included in the invention are primers AAF9317 - AAF89429 and AAB88419. Included in the invention are primers AAF9317 - AAF894295 and AAF82223 - AAF82232 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples.
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11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00183766.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify medulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (BLISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes
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                                                                                                                                                    AsplysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla
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CTAGTGCTTGCTCCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA
                                                                                 AGGTATGTGAAGGCCTTCCCTTTTACAACAAGAATCAGCAGAAGGAAATGATCGAAACC
                                          ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
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Conservative: Mismatches: Indels: Matches:

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Local Similarity: Percent Similarity:

Best

Query Match:

Alignment Scores:

No.:

Gaps:

us-10-079-111-1.olig.rng

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Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; notropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; muscular dystrophy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
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                                                                                                                                                                                                        Human signal peptide containing protein HSPP-64 cDNA SEQ ID NO:198
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98US-0094983P.
98US-0102686P.
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                             AAZ98172 standard; cDNA; 2029
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1023 AAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT 1082 AsplysasnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320 160 180 200 260 100 140 602 722 220 242 243 Griccaaggerichtrigegrigeagaaggerintecareeaggrigheargaarnargggg 302 362 422 482 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120 902 80 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGGGGCTCCTG 303 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile AGCCCAAACCCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle GAATITATIGICAGIGACAGIACCIACICGGIGGCATCCCCTIACITACAATACCIGCC ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLySLySLeuIle CCTACTACTACTACTCCTCCTCCTCCACCTTCTATTCCACGGGAAAAATTGATT CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal GluAsnLysAlaAlaPheLysAsnGluAlaAlaAlaGlyPheGlyGlyValProThrAlaLeu 963 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACC reragecrecregeacraagriregecegeaaggaccaagrigaaacagccrreaaagcr AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACA LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys cradification contraction and c LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly x AAZ98172 (1-2029) US-10-079-111-1 (1-322) 183 543 723 241 903 281 21 41 363 423 101 483 121 141 603 663 181 201 783 221 843 261 301 61 81 161 ò 셤 ò qq à g à g à g à qq à d ð qq à qq ò d ð d à g à 셤 à g ð d

thuman signal peptide-containing proteins HSPP-1 to HSPP-144. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, cardiovascular and antiaschmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP associated with increased activity or function of HSPP. Such diseases include cell proliferation activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, caproductive or developmental disorders, (e.g. arteriosclerosis, circhosis, psoriasis, acquired immune deficiency syndrome, anaemia, crhom's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's circhosis, cands can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for detecting HSPP in standard hybridisation and amplification assays and for chromosomal mapping. HSPP are also used to raise corribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP related diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP from naturals.

Seguence 2029 BP; 612 A; 463 C; 445 G; 509 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A new cDNA encoding a protein differentially expressed in breast cancer designated PCEBC is useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated cDNA encoding a protein that is differentially expressed in breast cancer, designated PDEBC. The invention is useful to diagnose breast cancer. The invention is also useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of the disease. The present sequence represents cDNA encoding human PDEBC Incyte 3044710CB1. Note: There are two sequences that have been assogned SEQ ID 2 in the sequence listing.
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Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair; ss.
Protein PRO263 cDNA clone DNA34431-1171
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97US-0059115P.
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Yuan J;

Chen J,

Pennica D,

Goddard A,

Gurney AL,

Wood WI,

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AAX52213-74 encode secreted and transmembrane human proteins, and are obtained from cDNA libraries prepared from fetal lung, fetal kidney, tetal brain, fatal luver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PR021 and PR0217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus arrophy), skin diseases associated with abnormal Reratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of twilva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including PR0265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PR0264 can be used as a target for anti-tumor drugs. PR0533 may be used as an anti-thrombotic agent; PR0287 polypeptides and portions may be used for treating problems of the kidney, uterus, endometrium, can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract
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                                                 New isolated human genes and polypeptides used in,
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Mismatches:
Indels:
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WPI; 1999-229533/19.
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                  P-PSDB; AAY13379
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SEQ ID NO 200; 355pp; English.
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Best Local Similarity:
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GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
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transmembrane polypeptides with
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                                                                                                                                                      The invention relates to a novel nucleic acid encoding a PRO polypeptide.
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Novel nucleic acids encoding secreted and transmembrane homology, e.g. to growth and cancer-associated antigens.
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Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
                                                                                                                                                                                                                                                          The present sequence is one of sixty one nucleic acids encoding novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin, diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma, gastrointestinal disorders (e.g. lung enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids
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ldi CJ, Gurney AL,
Paoni NF, Roy MA,
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                  Godowski PJ, Grim
Mather JP, Pan J,
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                                                  Williams PM,
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                                                                                                     GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTG
                                                                                                                                          LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
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CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
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99US-0145698P.
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99WO-US020594.
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15-SEP-1999;
05-OCT-1999;
29-NOV-1999;
30-NOV-1999;
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Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and
                                                                                                                                                                           The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu
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    Godowski
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   Goddard A,
Wood WI;
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Matches:
Conservative:
Mismatches:
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   Gerritsen M
Watanabe O
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P-PSDB; AAB87528.
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15-SEP-1999; 99WO-US021090.
07-DEC-1999; 99US-0169495P.
09-DEC-1999; 99US-0170262P.
11-JAN-2000; 2000WS-0175481P.
11-JAN-2000; 2000WO-US004342.
22-FEB-2000; 2000WO-US004414.
01-MAR-2000; 2000WO-US005601.
01-MAR-2000; 2000WS-019102P.
21-MAR-2000; 2000WS-0191007P.
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22-MAY-2000;
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01-JUN-2001; 2001WO-US017800.
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2001WO-US021066.
2001WO-US021735.
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Grimaldi JC, Gurney AL,
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10-NOV-2000; 2
01-DEC-2000; 2
20-DEC-2000; 2
28-FEB-2001; 2
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18-FEB-2000; 2
01-MAR-2000; 3
30-MAR-2000; 2
22-MAY-2000; 2
23-AUG-2000; 2
25 - JUN - 1998,
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24-SEP-1998;
24-SEP-1998;
30-SEP-1998;
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08-MAR-1999;
14-MAY-1999;
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01-SEP-1999;
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                                                                                                                                                   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
                                                                                                                                                                                                                                                                           1000 AAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT
                                                                                                                                                                                                                                                                                                                 AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla
                                                                                                                                                                                                                                                                                                                                                1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAAGCT
              CyeValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                                          760 rerereacadaderritraregadaecradeacedrereracadadaecredaecentrerr
                                                                                                      820 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
                                                                                                                                   LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
                                                                                                                                                                                               ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
                                                                        GluAenLysAlaAlaPheLysAenGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA encoding secreted/transmembrane protein PRO263
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98US-008479F

98US-0083495F

98US-008879F

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04-JUN-1998;
10-JUN-1998;
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10-JUN-1998;
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16-JUN-1998;
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29-OCT-1997;
22-APR-1998;
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Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
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WPI; 2002-731348/79.

DR P-PSDB; ABG958B3.

XX
New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis.

XX
XX
Claim 2; Fig 5; 399pp; English.

C The invention relates to an isolated secreted and transmembrane PRO CC Polypeptide having 80 % sequence identity to a sequence appearing as CC Polypeptide having 80 % sequence identity to a sequence of an RBG9581-ABG95834 or their associated signal peptide, or a sequence of an

custing its associated signal peptides. Also included are the nucleic acids encoding the proteins, vectors, host cells, fusion proteins and antibodies which specifically bind to the proteins. The proteins are nutibodies which specifically bind to the proteins. The proteins are useful for detecting, polypeptide designated as A, B, C or D in a sample subspected of containing an A, B, C or D polypeptide, by contacting the sample which a polypeptide designated as B, F, G, H or I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is the sample, where the formation of the conjugate is the sample, where the formation of the conjugate is a RR010272 polypeptide, B is a RR02010 polypeptide, C is a RR010376 polypeptide, B is a RR02010 polypeptide, C is a RR01096 polypeptide, D is a RR019976 polypeptide, The sample conjugate in the sample of the conjugate in the sample where the formation of the conjugate is a RR019976 polypeptide, C is a RR019976 polypeptide, The Signal State of the C is a cell suspected of expressing the A, B, C or D polypeptide, The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I The broactive molecule is a toxin, a radiolabel or an antibody. The broactive molecule causes death of the cell. A, B, C, D, E, F, G, H, or I The broactive molecule is a toxin, a radiolabel or an antibody c activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I The treatment of a condition which is responsive to the custivity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I The antipodies against them are useful for moterial and subject of the proteins are useful as therepeutic agents for treating sponsive to the proteins, are useful as the protein and plan and plan and gene are useful as a useful and eventual and soreening of therapeutic neared and ev extracellular domain of the proteins with their associated signal or lacking its associated signal peptide. Also included are the macids encoding the proteins invention

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 2372 322 0 0 0 0 Length:
Matches:
Conservative:
Mismatches: Indels: Gaps: x ABS74380 (1-2372) 1.49e-304 322.00 100.00% 100.00% US-10-079-111-1 (1-322) Similarity: Percent Similarity: Best Local Similari 21 220 Query Match: DB: No.: à g δ Ω ⋧ g

ATGECCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle 100 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla ValGinGlySerLeuArgAlaGluGluLeuSerIleGinValSerCysArgIleMetGly 100 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTTAGGATT 81 61 ò g 8 임

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20-JUN-2001; 2001WO-US019692.

| SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal 120

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AAAGTAGTAAAGGAGGAGGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT 1059 1060 GATAAAAACCCAGAAGAGTCCAAGGAAAACTACCGTGCGATGCCTGGAAACT 1119 180 160 639 669 200 759 220 240 280 AGCCCAAACCCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG 519 260 vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss. 580 CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACAACAACAACA ProThrThrThrProProAlaProAlaSerThrSerIleProArqArqLysLysLeuIle 880 CTAGTGCTTGCTCTCCTCTTTTGGTGCTGCTGCTGGTCTTGGATTTTGCTATGTCAAA 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaAlaGlyLeuGlyPheCysTyrValLys CCTACTACTACTCCCCCCCCCCCCCCTCCCACTTCTATTCCACGAGAAAAAATTGATT CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu GAAATTAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGGATACTTGGACTAACTCGTGCATT ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr Human; angiogenesis; cardiant; cytostatic; antiangiogenic; Human PRO263 cDNA sequence SEQ ID NO:31. BP. ABL88087 standard; cDNA; 2372 (first entry) 1120 GAAGTT 1125 GluVal 322 sapiens. 16-MAY-2002 760 0001 460 141 161 181 700 201 820 241 261 301 321 121 221 10 Homo ABL88087 g 8 6  $\dot{\delta}$ q à qq ò g ò g δ a Š g ò a ò qq 8 q ਨੇ

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SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angiogenesis (such as breast cardinoma and liver cardinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use an hybridisation probes, and in chromosome and gene mapping. ABL88252 to ABL88267 represent primers and probes used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paoni NF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              errara N, Gerber H, Gerritsen ME, Goddard A;
Gurney AL, Hillan KJ, Marsters SA, Pan J,
Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2372
322
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mapping. ABL88259 to ABL88267 represent E
exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 31; 565pp; English.
                                                                                                                                                                                                                                                                                                                     24 - CCT - 2000, 2000US - 02429229.
08 - NCV - 2000, 2000US - 02429229.
08 - NCV - 2000, 2000WS - 02429229.
10 - NCV - 2000, 2000WS - 0330873.
01 - DEC - 2000, 2000WS - 032678.
20 - DEC - 2000, 2000WS - 032678.
20 - DEC - 2000, 2000WS - 032678.
22 - JAN - 2001, 2001US - 00796498.
28 - FEB - 2001, 2001US - 00796498.
28 - FEB - 2001, 2001US - 0086689.
29 - MAR - 2001, 2001US - 00808689.
20 - APR - 2001, 2001US - 00816889.
20 - APR - 2001, 2001US - 00816889.
20 - APR - 2001, 2001US - 00816889.
20 - APR - 2001, 2001US - 0081689.
21 - MAY - 2001, 2001US - 008164280.
22 - MAY - 2001, 2001US - 008164280.
23 - MAY - 2001, 2001US - 008164280.
25 - MAY - 2001, 2001US - 008164280.
                                                                                                                                                                                     2000WO-US023522.
2000WO-US023328.
2000US-0230978P.
2000US-00664610.
2000US-00665350.
                                                                                                           2000WO-US020710
2000US-0222695P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001WO-US017092.
30-MAY-2001; 2001US-00870574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.49e-304
322.00
100.00%
100.00%
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30-MAY-2001; 2001WO-US017443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001; 2001WO-US017800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferrara N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-090516/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABB84832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
23-JUN-2000;
20-JUL-2000;
25-JUL-2000;
28-JUL-2000;
28-JUL-2000;
17-AUG-2000;
17-AUG-2000;
23-AUG-2000;
24-AUG-2000;
24-AUG-2000;
24-AUG-2000;
24-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baker KP, Fe
Godowski PJ,
                                                                                                                                                                                                                                                                       18-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stephan JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
     8 \times 6 ```

80

1119

819

240

260

200

```
Alignment Scores:
                          Baker KP,
   280
  61
   340
  81
   400
   101
   460
  191
   640
  121
   Query Match:
à
  d
  ð
   g
   à
   g
   à
  g
   à
   q
  ò
  a
  ò
   g
  à
   qq
   ð
   g
  Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; thereroslerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; gene; ss.
  Human angiogenesis related cDNA PRO263 SEQ ID NO: 31
                ВР
   10-NOV-2000; 2000MO-US930873.

10-NOV-2000; 2000MO-US932678.

20-DEC-2000; 2000MO-US932678.

20-DEC-2000; 2000MO-US934956.

22-JAN-2001; 2001US-00767699.

28-FEB-2001; 2001US-00766498.

28-FEB-2001; 2001WO-US906666.

01-MAR-2001; 2001WO-US906666.

14-MAR-2001; 2001US-00808689.

22-MAR-2001; 2001US-00808689.
   28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
09-MAR-2001; 2001WS-00802706.
14-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-00854280.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00854280.
  25-MAY-2001; 2001US-00866028.
25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001WG-US017092.
30-MAY-2001; 2001US-00870574.
30-MAY-2001; 2001WG-US01743.
01-UNN-2001; 2001WG-US017800.
20-UUN-2001; 2001WG-US017800.
               ABL95576 standard; cDNA; 2372
   25-JUL-2000; 2000US-0220624P.
25-JUL-2000; 2000US-0220664P.
28-JUL-2000; 2000WO-US020710.
   02-AUG-2000; 2000US-0222695P.
17-AUG-2000; 2000US-00643657.
23-AUG-2000; 2000WO-US023522.
  24-AUG-2000; 2000WO-US023328.
07-SEP-2000; 2000US-0230978P.
18-SEP-2000; 2000US-00664610.
18-SEP-2000; 2000US-00665350.
  2000US-0242922P.
2000US-00709238.
2000WO-US030952.
   09-JUL-2001; 2001WO-US021735
   (first entry)
   GODDARD A.
GODDARI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
PAN J.
PAONI N F.
STEPHAN J F.
WATANABE C K.
  GERRITSEN M E.
  GENENTECH INC
  BAKER K P.
FERRARA N.
  WO200208284-A2
   18-SEP-2000; 2
18-SEP-2000; 2
24-OCT-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
  Homo sapiens
  19-JUL-2002
   31-JAN-2002
                                 ABL95576;
  (GERR/)
(GODD/)
(GURN/)
(HILL/)
(MARS/)
(PANJ/)
(PAON/)
(STEP/)
  (GETH )
(BAKE/)
(FERR/)
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```
339
   399
  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle 100
   459
  120
   519
  140
   The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention
   160 ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219
   279
   579
   669
   20
  40
   9
  80
  ATCACCCTTGTGGGAAAAAAGGCGAACCAGCTGAATTTCACAGAAGCTAAGGAGCCC
   1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu
   220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
  TGTAGGCTGCTGGGAGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
  AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTGTCTTGGAATTGGAAGGTTCCAGTG
   SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
   GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
   GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACATAACCTGCC
  21 ValGlnGlySerLeuArgAlaGluGluLeuSerlleGlnValSerCysArglleMetGly
   41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
  AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT
  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
  520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGGTACTTGGACTAACTCGTGCATT
  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
  Gerber H, Gerritsen ME, Goddard A;
L, Hillan KJ, Marsters SA, Pan J, Paoni NF;
CK, Williams PM, Wood WI, Ye W;
   One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
  Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
   2372
322
0
0
0
  Length:
Matches:
Conservative:
Mismatches:
Indels:
  Gaps:
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  Claim 1; Fig 31; 567pp; English.
  1.49e-304
322.00
100.008
100.008
100.008
  Godowski PJ, Gurney AL,
Stephan JF, Watanabe CK,
   Ferrara N,
(WILL/) WILLIAMS P M. (WOOD/) WOOD W I.
   WPI; 2002-171999/22
  Percent Similarity:
Best Local Similarity:
  P-PSDB; ABB95438
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Ferrara N;
ME, Goddard A;
Kljavin IJ;
   Desnoyers L, Eaton DL,
W, Gerber H, Gerritsen
Gurney AL, Hillan KJ,
NF, Roy MA, Stewart TA,
   Ashkenazi A, Botstein D, Desnoyers L, Filvaroff E, Fong S, Gao W, Gerber H Godowski DJ, Grimaldi JC, Gurney AL, Mather JP, Pan J, Paoni NF, Roy MA, Williams PM, Wood WI;
   13 - SEP - 1999 ; 99W0-USG220945 ; 15 - SEP - 1999 ; 99W0-USG22094 ; 15 - SEP - 1999 ; 99W0-USG22094 ; 15 - SEP - 1999 ; 99W0-USG22094 ; 29 - NOV - 1999 ; 99W0-USG22094 ; 29 - NOV - 1999 ; 99W0-USG2814 ; 20 - DEC - 1999 ; 99W0-USG2813 ; 16 - DEC - 1999 ; 99W0-USG2856 4 ; 16 - DEC - 1999 ; 99W0-USG2856 4 ; 16 - DEC - 1999 ; 99W0-USG3091 ; 20 - MAR - 2000 ; 20 00W0-USG3084 ; 20 - MAR - 2000 ; 20 00W0-USG312 ; 20 - DEC - 2000 ; 20 00W0-USG332 ; 20 - DEC - 2
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9705-0063121P
9705-0063121P
9705-0063329P
9705-0063329P
9705-0063544P
9705-0063544P
9705-0063564P
9705-0063564P
9705-0063564P
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9705-0063734P
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9705-0064216P
9705-00664103P
9705-00664103P
9705-00664103P
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9705-00664103P
9705-00664103P
9705-00664103P
9705-00664103P
9705-00664103P
  98WO-US018824.
98WO-US019177.
  98WO-US025108.
99WO-US020594.
   98WO-US019330.
98WO-US019437.
   2000US-00665350
  (GETH ) GENENTECH INC.
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
27-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
29-0CT-1997;
20-0CT-1997;
20-0C
     X
  1059
   1119
  Human, PRO; gene; ss; secreted polypeptide; transmembrane polypeptide; pathological disorder; cardiac insufficiency disorder; protein secretion; pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis; skin disease; keratinocyte differentiation; epithelial cancer; tumour; lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma; cytostatic; cardian; endocrine; antidiabetic; gastrointestinal; antiulcer; dermatological; vulnerary.
  AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
  ProThrThrThrProProAlaProAlaSerThrSerlleProArgArgLysLysLeulle
                               CCTACTACTACTCCTCCTCCTCCTCCTCCTCTTCTATTCCACGGAGAAAAATTGATT
   GluAsniysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
  GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCCAGGGTCTG
  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
   261 ArgTyrVallysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  AGGTATGTGAAGGCCTTCCCTTTTACAACAAGAATCAGCAGAAGGAAATGATCGAAACC
   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
  AAAGTAGTAAAAGGAGGAGGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAAAACT
  GATAAAAACCCAGAAGAGTCCCAAGAGCTCCAAAACTACCGTGCGATGCCTGGAAGCT
  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
  crasifectricerecterretries recreated as a construction of the const
   970S-0059113P.
970S-0059115P.
970S-0059117P.
970S-0059121P.
970S-0059122P.
970S-0059124P.
970S-0059268P.
970S-0062285P.
970S-0062285P.
970S-0062287P.
970S-0062287P.
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  US2002146709-A1.
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24-OCT-1997;
24-OCT-1997;
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17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
   16-JUN-2003
  10-OCT-2002
   880
  940
  281
  1000
   301
  700
   201
   260
   221
  241
   321
  ACA59060;
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759

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LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTytValLys
  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
   AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
   1060 GATAAAAACCCAGAAGAGTCCAAGAACTCCAAGCAAAACTACCGTGCGATGCCTGGAAGGT
  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
   GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
   CTAGTGCTTGCTCTCTTTTTTGTGCTGCTGCTGGTCTTGGATTTTTGCTATGTCAAA
   AGGIATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
  AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT
  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
   ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  Human, secreted and transmembrane protein, PRO polypeptide, cancer,
Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
  cDNA encoding human PRO polypeptide #36.
  BP.
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97US-0059113P
97US-0059113P
97US-0059121P
97US-0059122P
97US-0059164P
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97US-0062287P
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  97US-0063121P.
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97US-0063128P.
   2001US-00902853
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  US2002192659-A1.
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   10-JUN-2003
   24-OCT-1997;
   17-SEP-1997
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  24-OCT-1997
24-OCT-1997
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  301
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   1120
   221
  201
   RESULT 13
  ACA58457
  g
  P
   à
  gg
   qq
  à
   Db
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   à
   8
   The invention relates to human PRO polypeptides (secreted or transmembrane polypeptides) and the polymucleotides encoding them. The PRO polypeptides and polynucleotides can be used in treating pathological disorders and tumours, in therapeutic treatment of cardiac insufficiency disorders and in therapeutic treatment of disorders involving protein secretion by the pancreas, including diabetes. They can also be used in treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, and skin diseases associated with abnormal keratinocyte differentiation (e.g., psoriases, epithelial cancers such as lung squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas). The sequences can be used as molecular markers for protein binding electrophoresis purposes and can be utilised in protein-protein binding massays, biochemical screening assays, immunoassays and cell-based assays.
  459
   669
   219
   279
  339
   399
   100
   SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
   AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 519
  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
  579
   ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
  639
  GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
  181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle 200
  80
  40
   9
   20
  Isolated nucleic acid useful for e.g., treating pathological disorders encodes a secreted or transmembrane protein.
  ATGCCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGGGGCTCCTG
   GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
  ATCACCCTTGTGAGGCAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
   TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAAAGCTTGAAAGGCT
   SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
   AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT
   GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
   Met Ala Arg Cys Phe Ser Leu Val Leu Leu I hur Ser I le Trp Thr Arg Leu Leu
  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArglleMetGly
   IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
   This sequence represents a human PRO polynucleotide of the invention
  BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
  2372
322
0
0
0
   Conservative:
Mismatches:
Indels:
  Length:
Matches:
  Gaps:
  US-10-079-111-1 (1-322) x ACA59060 (1-2372)
   2; Fig 73; 473pp; English
   1.49e - 304
  322.00
100.00%
100.00%
     2003-328338/31
   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                      P-PSDB; ABU71625
  Sequence 2372
  Alignment Scores:
Pred. No.:
  520
   141
  580
  161
   160
   220
  280
   340
  400
   460
  121
  21
  41
  61
   81
   101
   Claim
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97105 0063329P
97105 0063541P
97105 0063544P
97105 0063550P
97105 0063550P
97105 0063733P
97105 0063733P
97105 0063733P
97105 0063733P
97105 0063733P
97105 0063734P
97105 0063734P
97105 0063734P
97105 0064103P
97105 0064103P
97105 0064103P
97105 0064103P
97105 0064103P
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97105 0066120P
97105 0066120P
97105 0066120P
97105 0066120P
97105 0066120P
  98WO-US018824,
   99WO-US028564.
99WO-US028565.
  2000WO-US008439.
2000WO-US014042.
2000WO-US015264.
  98WO-US019177
98WO-US019330
  98WO-US019437
98WO-US025108
   99WO-US021547
  99WO-US028214
   99WO-US028313
99WO-US028301
   99WO-US020594
   99WO-US020944
   99WO-US021090
  99WO-US030999
   2000WO-US003565
  2000WO-US004414
  2000WO-US005841
   28-JUL-2000; 2000MO-US020710.
24-AUG-2000; 2000MO-US023328.
   99WO-US030911
  2000WO-US005004
  2000WO-US007377
   2000US-00665350
  2000WO-US0
   05-JAN-2000; 2
11-FEB-2000; 2
24-FEB-2000; 2
02-MAR-2000; 2
30-MAR-2000; 2
30-MAR-2000; 2
32-MAY-2000; 2
      27-OCT-1997;
28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
   15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
  14-SEP-1998;
16-SEP-1998;
  17-SEP-1998;
01-DEC-1998;
   30-NOV-1999;
01-DEC-1999;
   08-SEP-1999
   13-SEP-1999
   29-NOV-1999
   02-DEC-1999
   03-NOV-1997
  07-NOV-1997
   12-NOV-1997
   17-NOV-1997
  18-NOV-1997
   21-NOV-1997
  21-NCV-1997
  24-NOV-1997
   24-NOV-1997
   24-NOV-1997
  24-NOV-1997
  24-NOV-1997
  20-DEC-1999
```

## (GETH ) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Wood WI; Williams PM,

200

759

TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTGTT 819

CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal

cenaciaerecerecereceaecirecaericeairenaireaeaeaaaarigair

700

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760

201

ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle

2003-361832/34. P-PSDB; ABU71480 New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in

```
219
  279
  339
  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArglle 100
   120
  519
   140
   459
   579
  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
   639
  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
  669
   40
   09
  80
   The present invention relates to the isolation of novel human secreted sequences encoding them. The polypucledide sequences are useful in molecular biology, as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide sequences may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals of knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or their antibodies are useful in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as cancer. Alzheimer's disease or ischaemia, and in various disgnostic assays. The present sequence encodes a human PRO polypeptide of the invention
   160 ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCCATCTGGACCACCAGGCTCCTG
   220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
   460 AGCCCAAACCCCAAGTGTGGGGAAAAATGGGGTGTGTCCTGATTGGAAGGTTCCAGTG
  AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
   41 ileThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
  280 ATCACCCTTGTGAGCAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
  1 MetAlaArgCysPheSerLeuValLeuLeuLhrSerIleTrpThrArgLeuLeu
  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
   340 TGTAGGCTGCTGGGACTAGGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
   400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT
   SerProAsnProLysCysGlyLysAsnGlyValGlyValGeuIleTrpLysValProVal
   SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
  21 ValGinGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArglleMetGly
   CCAGAAATTATCACCACCACAAGATCCCATATTCAACACTCAAACTGCAACACAACAACAACA
  GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTACAATACCTGCC
  BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
 generating antisense RNA and DNA, and in gene therapy
  2372
322
0
0
0
0
  Length:
Matches:
Conservative:
Mismatches:
Indels:
   Gaps:
  US-10-079-111-1 (1-322) x ACA58457 (1-2372)
                                    2; Fig 73; 474pp; English.
  1.49e-304
322.00
100.00%
100.00%
  Similarity:
   Percent Similarity:
Best Local Similarit
  Sequence 2372
   Alignment Scores:
  61
  81
   121
   520
  141
  161
  640
   101
   580
   Query Match:
                                    Claim
  Pred. No.:
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   q
  ð
   g
   ò
  g
   ò
  a
  ò
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  à
   qq
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The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding
  New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, in generating probes and in tissue typing.
   Claim 2; Fig 73; 484pp; English
  WPI; 2003-329602/31.
P-PSDB; ABU71926.
28-0CT-1997;
29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
31-0CT-1997;
31-0CT-1997;
31-0CT-1997;
31-0CT-1997;
31-0CT-1997;
31-0CT-1997;
31-0CT-1997;
   GATAAAAACCCAGAAAGAGTCCAAGAGCCAAAACTACCGTGCGATGCCTGGAAGCT 1119
   1000 AAAGTAGTAAAGGAGGAGAGAGCCAATGATGAACCAACCTAATGAGGAATCAAAGAAACT 1059
                   240
  879
  260
   939
   280
   999
  300
  AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
                  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
   GAAAATAAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
   ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
   940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATGATGGAAAACC
  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaAlaGlyLeuGlyPheCysTyrValLys
   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr
   Human; ss; gene; secreted protein; transmembrane protein; PRO; gene therapy; chromosome identification; chromosome marker.
   Human cDNA for secreted/transmembrane protein PRO263.
  ACA60164 standard; cDNA; 2372 BP.
  970S-0059113P.
970S-0059115P.
970S-0059119P.
970S-0059121P.
970S-0059121P.
970S-0059122P.
970S-0059263P.
970S-0062287P.
970S-0062287P.
970S-0062287P.
970S-0062387P.
970S-0062387P.
970S-006387P.
970S-006387P.
970S-006387P.
970S-006387P.
970S-006387P.
970S-006387P.
970S-0063120P.
970S-0063120P.
970S-0063128P.
970S-0063128P.
970S-0063128P.
970S-0063128P.
   11-JUL-2001; 2001US-00904011
  12-JUN-2003 (first entry)
  GAAGTT 1125
   GluVal 322
  US2003003530-A1.
   15-0CT-1997)
17-0CT-1997)
21-0CT-1997)
24-0CT-1997)
24-0CT-1997)
24-0CT-1997)
24-0CT-1997)
24-0CT-1997)
24-0CT-1997)
24-0CT-1997)
24-0CT-1997)
   28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
  Homo sapiens.
   17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
  17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
   17-SEP-1997;
18-SEP-1997;
18-SEP-1997;
   28-OCT-1997
28-OCT-1997
  02-JAN-2003
  301
  1120
  820
   880
  ACA60164;
   281
   321
  241
  ACA60164

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Desnoyers L, Eaton DL, Ferrara N;

W, Gerber H, Gerritsen ME, Goddard A;

Gerrney AL, Hillan KJ, Kljavin IJ;

ROY MA, Stewart TA, Tumas D;
   Ashkenazi A, Botstein D, Desnoyers L, Filvaroff E, Fong S, Gao W, Gerber H, Godowski PJ, Grimaldi JC, Gurney AL, Mather JP, Pan J, Paoni NF, Roy MA, Williams PM, Wood WI;
  99WO-US030999.
2000WO-US000219.
2000WO-US003565.
  2000WO-US015264.
2000WO-US020710.
2000WO-US023328.
2000US-00665350.
97US-0063564P.
97US-0063435P.
97US-0063734P.
97US-00637334P.
97US-0063735P.
97US-0063735P.
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97US-0063735P.
97US-0063735P.
97US-0063735P.
97US-0063735P.
97US-00648P.
97US-00648P.
97US-00648P.
97US-00648P.
97US-006646P.
97US-0066453P.
  99WO-US028313.
99WO-US028301.
99WO-US028564.
  99WO-US023089.
  2000WO-US008439.
2000WO-US014042.
   99WO-US020594.
  99WO-US021090.
  99WO-US028565.
  2000WO-US004414.
   2000WO-US005004
  2000WO-US005841
   2000WO-US007377
  (GETH ) GENENTECH INC.
   01-DEC-1999;
02-DEC-1999;
16-DEC-1999;
16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
20-DEC-1999;
20-DEC-1999;
211-FEB-2000;
22-FEB-2000;
22-FEB-2000;
23-MAR-2000;
20-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
  21-NOV-1997;
21-NOV-1997;
24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
   02-JUN-2000;
  24-AUG-2000;
18-SEP-2000;
   17-SEP-1998;
01-DEC-1998;
  15-SEP-1999;
15-SEP-1999;
  05-OCT-1999;
29-NOV-1999;
   17-NOV-1997
18-NOV-1997
  24-NOV-1997
  10-SEP-1998
   16-SEP-1998
  08-SEP-1999
   13-SEP-1999
   30-NOV-1999
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the PRO protein extracellular domain. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the vector, producing a PRO polypeptide (by culturing the host cell for the expression of the PRO polypeptide, and recovering the PRO polypeptide from the cell culture), an isolated PRO polypeptide (having at least 80% sequence identity to: (2 a namino acid sequence selected from the 61 PRO proteins; (D) an amino acid sequence encoded by a nucleic and molecule deposited with an ATCC number (detailed in the specification); or (c) an extracellular domain of a PRO polypeptide or to a PRO polypeptide of fused to a certain an extracellular domain of peptide), a chimaeric molecule comprising a PRO polypeptide of fused to a checklogous amino acid sequence, an anti-PRO antibody, detecting a pro245 or PRO1868 in a sample suspected of containing the polypeptide, Inking a bloactive molecule to a cell expressing a PRO245 or PRO1868. Nucleic acids which encode PRO can be used to generate either transgent animals or knock-out animals which may be used in the molecule. development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The present sequence encodes a PRO protein 

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

100 279 399 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal 120 519 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140 579 639 GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180 669 40 9 80 220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG MetAlaArgCygPheSerLeuValLeuLeuLhrSerIleTrpThrThrArgLeuLeu CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle 400 AGCTTTGAAACTTGCAGCTATGGCTGGGGTTGGAGATTCGTGGTGGTCATCTCTAGGATT ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT AGCCCAAACCCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 2372 322 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: US-10-079-111-1 (1-322) x ACA60164 (1-2372) 1.49e-304 322.00 100.00% 100.00% 100.00% Local Similarity: Percent Similarity: Alignment Scores: 61 81 101 460 121 520 141 161 640 Query Match: ö 셤 ò ď Š g ਠੋ 셤 8 d ઠે 셤 ठ a ò qq ò

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Human; secreted and transmembrane protein; PRO; pharmaceutical; diagnostic; biosensor; bioreactor; Parkinson's disease; Alzheimer's disease; inflammation; nephritis; wound healing; nerve repair; collateral blood vessel formation; cancer; colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes; cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid; scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis; infertility; gene therapy; gene; ss.
   301 AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
  CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTAAA
   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
  1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGGAAGCT
ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle
                           ceracinetracicerecreerecreericeactreereringianicalegadaaaaaarrearr
  GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCCACGGCTCTG
   LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
   261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  940 AGGIATGIGAAGGCCTICCCTITIACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
  TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
   GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
  Novel human secreted and transmembrane protein PRO263 cDNA.
  BP.
   ACD07564 standard; cDNA; 2372
   97US-0059113P.
97US-0059117P.
97US-0059111P.
97US-0059121P.
97US-0059124P.
97US-0059164P.
97US-0059266P.
97US-0062125P.
97US-0062125P.
97US-006228FP.
97US-006228FP.
  17-JUL-2001; 2001US-00907824
  (first entry)
   1120 GAAGTT 1125
  GluVal 322
  US2002197671-A1
   Homo sapiens.
   17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
  07-AUG-2003
   26-DEC-2002.
  17-SEP-1997;
   21-OCT-1997
   18-SEP-1997
  18-SEP-1997
  17-0CT-1997
  15-OCT-1997
   17-0CT-1997
  820
  880
   281
                         700
  160
   ACD07564;
181
   201
   221
   241
  321
  RESULT 15
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97US-0062814P

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9705-0063550P-
9705-0063550P-
9705-0063704P-
9705-0063704P-
9705-0063734P-
9705-0063734P-
9705-0063734P-
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9705-0064215P-
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9705-0066453P-
9705-0066453P-
9705-0066453P-
9705-0066453P-
9705-0066453P-
9705-006651P-
9705-0066453P-
9705-006651P-
        97US-0062816P.
97US-0063045P.
97US-0063121P.
97US-0063121P.
97US-0063128P.
   97US-0063329P.
97US-0063541P.
97US-0063542P.
   24-FEB-2000; 2000WO-US005004
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
  98WO-US019177.
98WO-US019330.
   99WO-US028313.
  99WO-US028564.
  97US-0063544P.
  98WO-US019437
   98WO-US025108
   99WO-US020594
   99WO-US020944
   99WO-US021090
  99WO-US021547
   99WO-US023089
   99WO-US028214
   99WO-US028301
   99WO-US028565
   99WO-US030095
99WO-US030911
  99WO-US030999
  2000WO-US000219
  2000WO-US003565
   22-FEB-2000; 2000WO-US004414
  2000WO-US014042
  GETH ) GENENTECH INC.
  20-DEC-1999;
05-JAN-2000;
11-FEB-2000; 2
   15-SEP-1999;
05-OCT-1999;
29-NOV-1999;
  02-DEC-1999;
16-DEC-1999;
20-DEC-1999;
   22-MAY-2000;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
27-0CT-1997;
27-0CT-1997;
28-0CT-1997;
   29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
   28-OCT-1997;
28-OCT-1997;
   31-OCT-1997
   10-SEP-1998;
   14-SEP-1998
  17-SEP-1998;
   01-DEC-1998;
  08-SEP-1999
13-SEP-1999
  15-SEP-1999
   01-DEC-1999
  02-DEC-1999
  1997
   997
   18-NOV-1997
  21-NOV-1997
24-NOV-1997
  24-NOV-1997
  30-NOV-1999
  29-OCT-1997
29-OCT-1997
   07-NOV-1997
   NOV-1997
   24-NOV-1997
   NOV-1997
   OCT-1997
   31-OCT-1997
   28-OCT-1
  OCT-1
  28-OCT-
 oldsymbol{\mathsf{R}}
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Ferrara N; n ME, Goddard A; Kljavin IJ; Tumas D; Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Flvaroff E, Fong S, Gao W, Gerber H, Gerritsen Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA,

à В à

The invention describes a new isolated nucleic acid molecule comprising
the full length coding sequence of the DNA deposited with the American
the full length coding sequence of the DNA deposited with the American
conviction (e.g. ATCC Deposit No. 209258), or a sequence
with at least 80% identity to a DNA encoding a PRO polypeptide comprising
any of 61 sequences having 164-119 amino acids fully defined in the
specification. The PRO polypeptides or polynucleotides are useful as
particularly useful for detecting or treating e.g. Parkinson's disease,
contricularly useful for detecting or treating e.g. Parkinson's disease,
Alzheimer's disease, inflammations, nephritis, wound healing, nerve
conterly, haemorrhage (or reduce risk for hemorrhage), rheumatoid
cancer), haemorrhage (or reduce risk for hemorrhage), rheumatoid
carcer), haemorrhage (or reduce risk for hemorrhage), rheumatoid
carcer), haemorrhage (or reduce risk for hemorrhage), rheumatoid
conternis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
crestenosis, dermal fibrotic conditions (e.g. keloids or scarting),
cischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
therapeutic intervention in these diseases, and diagnostic determination
of the presence of these diseases. The PRO polypeptides are also useful
as molecular weight markers, or for chromosome identification. The PRO
censed are useful as hybridisation probes, or for screening libraries of
thuman cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
therapy, particularly for replacing a defective gene. This sequence
charapy, particularly for replacing a defective gene. This sequence New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO335), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia Claim 2; Fig 73; 482pp; English Williams PM, Wood WI; 2003-370793/35. P-PSDB; ABC01809 or strokes. 

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

|                                                                                            |                                             | hrArgLeuteu 20                                               | CGAGGCTCCTG 219                                                | rgileMetGly 40                                               | GAATTATGGGG 279                                               | laLysGluAla 60                                               | CTAAGGAGGCC 339                                              | laLeuLysAla 80                                               | CCTTGAAAGCT 399                                             | leSerArgile 100                           | TCTCTAGGATT 459                                               | ysValProVal 120                                              | AGGIICCAGIG 519                                              |
|--------------------------------------------------------------------------------------------|---------------------------------------------|--------------------------------------------------------------|----------------------------------------------------------------|--------------------------------------------------------------|---------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------|-------------------------------------------------------------|-------------------------------------------|---------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------|
| 2372<br>322<br>7e: 0<br>0                                                                  |                                             | MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu | ATGGCCAGGTGCTTCAGCCTGGTGTTTTTTTTCCACTTCCATCTGGACCACGAGGTCTCCTG | ValGinGlySerLeuArgAlaGluGluLeuSerIleGinValSerCysArgileMetGly | GTCCAAGGCTCTTTGCGTGCGAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG | IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla | ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGGTAAGGAGGCC | CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla | TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGGC | yrGlyTrpValGlyAspGlyPheValValIleSerArgIle | AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTGGTGGTCATCTCGTAGGATA | SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal | AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG |
| Length: Matches: Conservative: Mismatches: Indels:                                         | 1-2372)                                     | alleuleuleuThr                                               | rgrrgcrrcrcact                                                 | luGluLeuSerlle                                               | AAGAGCTTTCCATC                                                | laAsnGlnGlnLev                                               | CGAACCAGCAGCTG                                               | euAlaGlyLysAsp                                               | rggccggcaagga                                               | lyTrpValGlyAsp                            | GCTGGGTTGGAGAT                                                | ysAsnGlyValGly                                               | AAAATGGGGTGGGT                                               |
| 1,49e-304<br>322.00<br>100.00%<br>100.00%<br>100.00%                                       | US-10-079-111-1 (1-322) x ACD07564 (1-2372) | CysPheSerLeuVa                                               | TGCTTCAGCCTGG                                                  | SerLeuArgAlaG.                                               | TCTTTGCGTGCAG                                                 | ValSerLysLysA                                                | GTGAGCAAAAAGG                                                | LeuGlyLeuSerLe                                               | CTGGGACTAAGTT                                               | rsserT                                    | ACTIGCAGCTATG                                                 | ProLysCysGlyL)                                               | CCCAAGTGTGGGA                                                |
| res:<br>arity:<br>milarity:                                                                | -1 (1-322)                                  |                                                              |                                                                |                                                              |                                                               |                                                              |                                                              | _                                                            |                                                             | SerPheGluThrCy                            |                                                               |                                                              |                                                              |
| Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match: | -079-111                                    | 1                                                            | 160                                                            | 21                                                           | 220                                                           | 41                                                           | 280                                                          | 61                                                           | 340                                                         | 81                                        | 400                                                           | 101                                                          | 460                                                          |
| Alignment<br>Pred. No.<br>Score:<br>Percent S<br>Best Loca<br>Query Mate                   | US-10                                       | š                                                            | QQ                                                             | οy                                                           | Dp                                                            | ζ                                                            | qq                                                           | δ                                                            | οp                                                          | ķ                                         | d<br>d                                                        | δ                                                            | QQ                                                           |

121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

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  1059
   1119
   180
  669
   200
  220
   819
   240
  260
  759
   879
  939
  280
   999
   300
  320
ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle
                              eThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr
  CCAGAAATTATCACCACCACGAAAGATCCCATATTCAACTCTCAAACTGCAAACAACAA
   GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
  GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCygTyrValLys
   CTAGTGCTTGCTCCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTTGCTATGTCAAA
  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  LysvalvalLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
  AAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
  AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
   Human; secreted and transmembrane protein; PRO; antibody therapy; pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
   凡;
   Godowski
   secreted and transmembrane protein PRO263 cDNA.
   Goddard A,
Wood WI;
   ΩĔ,
   Gerritsen Matanabe (
  ВР
  2372
   01-MAY-2002; 2002US-00063515
   2001US-00006867
   (first entry)
  ACA91166 standard; cDNA;
   (GETH ) GENENTECH INC.
  Filvaroff
   Gurney
                             ProGlullell
  1120 GAAGTT 1125
  GluVal 322
  WPI; 2003-401702/38.
P-PSDB; ABU90878.
   US2003018173-A1
   Eaton DL, Fil
Grimaldi JC,
  06-DEC-2001;
  Homo sapiens.
   human
   11-JUL-2003
   23-JAN-2003.
   301
  580
   640
   181
   260
   820
   880
   261
  281
   321
                             141
  161
  700
   201
  221
  241
   ACA91166,
  Novel
  RESULT
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   ò
   셤
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The invention describes an antibody that specifically binds to a PRO polypeptide having a fully defined amino acid sequence given in the specification. The antibody is useful in identifying PRO polypeptides useful for various industrial applications, including pharmaceuticals, diagnostics, biosensors and bioreactors. The antibody is also used for affinity purification of PRO polypeptides from recombinant cell culture or natural sources. The antibody, PRO polypeptide, or its agonists or antagonists, may be used for preparing a medicament for diagnosing or treating a condition responsive to the antibody, PRO polypeptide, or its agonists. This sequence encodes a novel human secreted and transmembrane PRO polypeptide
                  New antibody useful for identifying PRO polypeptides, for affinity purification of PRO polypeptides, and for preparing a medicament for diagnosing or treating conditions responsive to the antibody or PRO
  English.
  5; 345pp;
   Disclosure; Fig
  polypeptide
```

0 U; 0 Other; 2372 322 0 0 0 Conservative: Mismatches: Indels: Τ; Length: Matches: BP; 721 A; 524 C; 489 G; 638 US-10-079-111-1 (1-322) x ACA91166 (1-2372) 1.49e-304 322.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Sequence 2372 gnment Scores: Query Match: DB: No.:

339 40 09 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla Grecaaggereragaaggerrecarceaggrerergeagaarrargggg ATCACCCTTGTGAGCCAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArglleMetGly 220 280 ч 21 41 61 ð g g ð ð g dC à

CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

180

GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla

```
20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WO-US034956.
22-MAR-2001; 2001WO-US036520.
22-MAR-2001; 2001US-00816744.
10-MAY-2001; 2001US-00854208.
30-MAY-2001; 2001US-00854208.
310-MAY-2001; 2001US-00870574.
01-JUN-2001; 2001WO-US017800.
  E,
  (GETH ) GENENTECH INC.
  Filvaroff
C, Gurney
  WPI; 2003-447384/42.
P-PSDB; ABO33937.
   Best Local Similarity:
   Percent Similarity:
  JC,
  06-DEC-2001;
   Alignment Scores:
  and cancer
  Eaton DL,
Grimaldi
   81
  Query Match:
DB:
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  1000 AAAGTAGTAAAGGAGAGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT 1059
  819
   240
   879
   LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
  939
  280
  999
  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
  320
  261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
   820 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCAGGGTCTG
   880 CTAGTGCTTGCTCTCTTTTTGTGCTGCTGGTCTTTGGATTTTGCTATGTCAAA
  AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
   gene; secreted/transmembrane protein; PRO; tumour; cancer;
   Human cDNA encoding secreted/transmembrane protein PRO263
   BP
  99KR-00062142.
99W0-02805028.
99W0-0311832.
99W5-00380137.
99US-00380138.
99US-00380142.
99US-00380142.
99US-00397342.
   ACD81543 standard; cDNA; 2372
  2000WO-US004341.
  2000US-00644848
2000WO-US023328
   2000WO-US030873
2000WO-US032678
   2002US-00063519
  99WO-US031274
  2000WO-US005601
  2000WO-US005841
  2000WO-US007532
  2000WO-US014042
  2000WO-US015264
  2000US-00664610
   2000US-00665350
   2000US-00709238
   entry)
  1120 GAAGTT 1125
   (first
  GluVal 322
   US2003009013-A1
   02-MAR-2000; 2
21-MAR-2000; 2
22-MAY-2000;
   24-AUG-2000;
18-SEP-2000;
18-SEP-2000;
08-NOV-2000;
10-NOV-2000;
01-DEC-2000;
  14-MAY-1999;
25-AUG-1999;
25-AUG-1999;
25-AUG-1999;
15-SPP-1999;
18-OCT-1999;
12-NOV-1999;
30-DEC-1999;
30-DEC-1999;
18-PEB-C-2000;
01-MAR-2000;
   02-JUN-2000;
22-AUG-2000;
   01-MAY-2002;
   Homo sapiens
   18-SEP-2003
   09-JAN-2003
  08-MAR-1999
  14-MAY-1999
   Human; ss;
   cytostatic
  281
   ACD81543;
                     260
   221
   241
  321
  301
  ACD81543
  RESULT
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The invention relates to an antibody that binds to a secreted or transmembrane protein designated PRO1446 appearing as ABO33941. The protein is one of 84 PRO polypeptides which (along with their encoding nucleic acids) are disclosed in the specification. The methods and compositions of the present invention are useful for the preparation of a medicament for the treatment of disorders associated with the aberrant expression or activity of the PRO polypeptide, such as tumour conditions and cancer. They can also be used to generate transgenic or knockout animals useful in the development and screening of therapeutically useful reagents. The PRO polypeptides and encoding nucleic acids can be used as molecular weight markers for protein electrophoresis, chromosome identification and tissue typing. The antibodies may be used in various diagnostic, competitive binding and/or immunoprecipitation assays. The present sequence encodes a PRO polypeptide
   SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle 100
  340 reradecrecreseacraagriresecesecaassaccaagricaaacasecricaaaser 399
  New isolated antibody specifically binding a PRO polypeptide, useful for the preparation of a medicament for treating disorders with the aberrant expression or activity of the PRO polypeptide, such as tumor conditions
   160 ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTACTTCCATCTGGACCACGAGGCTCCTG
  1 MetAlaArgCysPheSerLeuValleuLeuLhrSerIleTrpThrThrArgLeuLeu
   21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly
  220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
   41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
  61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
  ΡJ;
  Godowski
  Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
   2372
322
0
0
0
  Goddard A,
Wood WI;
  Conservative:
Mismatches:
Indels:
  Length:
Matches:
   Gerritsen ME,
Watanabe CK,
   US-10-079-111-1 (1-322) x ACD81543 (1-2372)
  Disclosure; Fig 5; 223pp; English.
   1.49e-304
322.00
100.00%
100.00%
29-JUN-2001; 2001US-00869599.
18-JUL-2001; 2001US-00908827.
  2001US-00006867
```

20

279

9

40

339

us-10-079-111-1.olig.rng

06-DEC-2001; 2001US-00006867.

```
1059
  1119
   320
   519
   140
  639
  180
   200
  220
  240
   579
   160
   669
  759
  819
   879
   260
  939
  280
  300
   Human, secreted and transmembrane polypeptide; gene; ss. chromosome mapping; gene mapping; transgenic animal; knockout animal; therapeutic agent screening; chromosome identification; tissue typing;
AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATTCGTGGTCGTCTCTAGGATT
   SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCyslle
  AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
   ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
  GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThr1leProAla
  GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
  CCTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT
  TGTGTCACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
  GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
   LeuValLeuAlaLeuLeuPheGlyAlaAlaAlaGlyLeuGlyPheCysTytValLys
  CTAGTGCTTGCTCCTCTTTTTGGTGCTGCTGCTCTTTGGTTTTTGCTATGCTATG
   ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
  AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
  GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT
  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
   GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
  AAAGTAGTAAAGGAGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
                          SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
   Novel human secreted and transmembrane protein PR0263 cDNA
   BP.
  ACA60365 standard; cDNA; 2372
  (first entry)
   1125
   GluVal 322
   GAAGTT
   US2003018183-A1
  gene therapy
  11-JUN-2003
   1000
                          101
  460
  121
   141
   580
   191
   640
   700
   260
   221
   261
   940
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  ACA60365
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01-MAY-2002; 2002US-00063512

23-JAN-2003

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The invention describes novel isolated PRO polypeptides. The PRO polypeptides or anti-PRO antibodies are useful in preparing a medicament for treating a condition that is responsive to the PRO polypeptide or antibody. The PRO nucleotide sequences may be used as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleotids are also useful in preparing PRO polypeptides, in sasys to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for protein electrophoresis therapy, and as molecular weight markers for protein electrophoresis curposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell
  279
  339
   399
  100
   459
  New secreted and transmembrane PRO polypeptides and nucleic acid molecules encoding the polypeptides, useful in gene therapy or preparing a medicament for treating a condition that is responsive to the PRO
   40
   09
   80
  AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT
   SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal
  MetAlaArgCysPheSerLeuValLeuLeuLhrSerIleTrpThrThrArgLeuLeu
  ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG
  Grccaaggcrcrrrgcgrgcagaagacrrrccarccaggrgrcargcagaarrarggg
  280 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
   340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
   SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
  520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
   ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
   IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
  CysArgleuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
  460 AGCCCAAACCCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
  P.C.;
  Godowski
   U; 0 Other;
  2372
322
0
0
0
  Goddard A,
Wood WI;
  Conservative:
Mismatches:
Indels:
  0
  .,
  Length:
Matches:
   489 G; 638
  Ã,9,
   US-10-079-111-1 (1-322) x ACA60365 (1-2372)
  Gerritsen
Watanabe
   Disclosure, Fig 5; 409pp; English.
   and transmembrane PRO poypeptide
   721 A; 524 C;
  1.49e-304
   322.00
100.00%
100.00%
  Ē,
ĀĽ,
  polypeptide or antibody.
                               (GETH ) GENENTECH INC
  Filvaroff
   Gurney
  WPI; 2003-330984/31
P-PSDB; ABU71954.
   best Local Similarity:
Query Match:
   Sequence 2372 BP;
  Percent Similarity:
  Eaton DL, Fi
Grimaldi JC,
  Alignment Scores:
  н
   160
  220
   41
   21
  61
  81
   400
   101
   121
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9705-0059121P.
9705-0059122P.
9705-0059184P.
9705-005284F.
9705-0062817P.
9705-0062816P.
9705-0062816P.
9705-0062816P.
9705-0062814P.
9705-0063120P.
9705-0063121P.
9705-0063121P.
9705-0063122P.
9705-0063122P.
9705-0063124P.
   99WO-US021090.
99WO-US021547.
99WO-US023089.
  99WO-US020594.
  2000WO-US014042.
2000WO-US015264.
2000WO-US020710.
   98WO-US019177.
98WO-US019330.
  98WO-US019437,
98WO-US025108,
   99WO-US028214
99WO-US028313
   99WO-US028301
99WO-US028564
  99WO-US028565.
   2000WO-US000219.
   2000WO-US003565.
2000WO-US004414.
   99WO-US030911
  99WO-US030999
  2000WO-US005004
   2000WO-US005841
   06-JAN-2000;
11-FEB-2000;
22-FEB-2000;
24-FEB-2000;
  22-MAY-2000;
02-JUN-2000;
28-JUL-2000;
   14-SEP-1998;
16-SEP-1998;
17-SEP-1998;
  02-DEC-1999;
16-DEC-1999;
20-DEC-1999;
                     17. SEP-1997;
18. SEP-1997;
18. SEP-1997;
15. OCT-1997;
17. OCT-1997;
24. OCT-1997;
  1997;
   1997;
  1997;
  1997;
   1997;
   24-NOV-1997;
   1997;
   1997;
   29-NOV-1999;
   1997;
  1997;
  13-SEP-1999,
  20-DEC-1999
   766
   766
   997
   1997
  1997
  01-DEC-1999
   02-DEC-1999
   766
  1661
  1997
  997
  997
  997
   997
   997
  997
   997
   997
  997
   997
   17-NOV-1
17-NOV-1
17-NOV-1
18-NOV-1
21-NOV-1
21-NOV-1
24-NOV-1
   24-0CT-1
27-0CT-1
28-0CT-1
28-0CT-1
28-0CT-1
28-0CT-1
28-0CT-1
29-0CT-1
20-0CT-1
20-0CT-1
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20-0CT-1
20-0CT-1
20-0CT-1
20-0CT-1
20-0CT-1
20-0CT-1
20-
   24-NOV-1
24-NOV-1
       1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT 1119
  1000 AAAGTAGTAAAGGAGAGAAAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGAAAACT 1059
  300
   AsplysAsnProGluGluSerlysSerProSerbysThrThrValArgCysLeuGluAla 320
  759
  280
  639
   180
  669
  200
   220
   819
  GluAsniysAlaAlaPheiysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
   879
   260
  939
   999
  GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCAGGGTTTG
   LeuValLeuAlaLeuDhePheGlyAlaAlaAlaAlaGlyLeuGlyPheCysTyrValLys
  261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
   940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
                            ProGlullelleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr
  CCAGAAATTATCACCACCACAAAGATCCCATATTCAACACTCAAACTGCAACACAACAACAACA
  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
  CCTACTACTACTCCTCCTGCTCCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT
  TGTGTCACAGAAGTTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
   640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
   CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
  Human; PRO; secreted protein; transmembrane protein; enterocolitis;
  gastrointestinal ulceration; skin disease; ss; gene; abnormal keratinocyte differentiation; psoriasis; epithelial cance abnormal keratinocyte differentiation; psoriasis; epithelial canceration carcinoma; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; inflammatory disease; rheumatoid arthritis; asthma; multiple sclerosis; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AlDS, acquired immunodeficiency syndrome; cancer; diabetic complication; wound repair.
  Human cDNA encoding secreted/transmembrane protein PRO263.
  BP
   97US-0059113P.
97US-0059115P.
97US-0059117P.
97US-0059119P.
  ABX71612 standard; cDNA; 2372
   2001US-00909320
   (first entry)
  1120 GAAGTT 1125
  GluVal 322
   US2002132240-A1
   17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
   18-JUL-2001;
   Homo sapiens
  10-MAR-2003
   19-SEP-2002
  880
  281
  580
  200
  160
   820
   241
   ABX71612;
  221
   301
  321
   161
  181
   201
   RESULT 19
ABX71612
XX
AC ABX71.
XX
DT 10-MAI
XX
DY HUMAN
XX
HUMAN
XX
HUMAN
XX
RW SQUAM
XW ABNOTT
XW ABNOTT
XW ABNOTT
XW ACC
XW A
```

```
Botstein D, Desnoyers L, Eaton DL,
Fong S, Gao W, Gerber H, Gerritsen
Grimaldi JC, Gurney AL, Hillan KJ,
an J, Paoni NF, Roy MA, Stewart TA,
Wood WI;
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
               (GETH ) GENENTECH INC.
  WPI; 2003-147434/14.
                         Ashkenazi A, Botst
Filvaroff B, Fong
Godowski PJ, Grima
Mather JP, Ban J,
Williams PM, Wood
  P-PSDB; ABU54382
```

Ferrara N; ME, Goddard A; Kljavin IJ; Tumas D; New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease

Claim 2; Fig 73; 473pp; English.

The invention relates to an isolated PRO polypeptide having at least 80% amino acid sequences given in the specification (appearing as ABU54347-caid sequences given in the specification (appearing as ABU54347-caid sequences given in the specification (appearing as ABU54347-caid sequences given in the specification); (c) any one of the PRO sequences which careful a sesociated signal peptide; (d) an extracellular domain of the PRO polypeptide with its associated signal peptide; (d) an extracellular domain of the PRO polypeptide which lacks its associated signal peptides. Also include are the nucleic acids encoding the PRO polypeptides and nucleic acids are useful in diagnosing or treating conference. The proposition of the PRO polypeptides and nucleic acids are useful in diagnosing or treating conferences such as squamous cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g. cancers such as squamous cell carcinoma, Alzheimer's disease, premature conferences are also useful for wound repair and associated therapies concerned with re-growth of fissue. The nucleotide sequences may be used as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA, PRO nucleic acids are also useful in proper and selective and sessociated herapies concerned with re-growth of fissue. The nucleotide sequences may be used as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA, PRO nucleic acids are also useful for volver roceins or missuely and proper proper and probes in chromosome and gene mapping, or in generating antisense RNA and DNA, PRO nucleic acids are also useful for yother proceins or missuely produced with re-growth of fissue. The nucleotide sequences may be used as shown the proceins or missuely and proceins and gene mapping, or in generating antisense RNA and DNA, properties are also useful for wollypeptides are also useful for yother proceins or missue proceins or missue proceins or mis polypeptides, in assays to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents. therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. The present sequence encodes PRO polypeptide

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

2372 322 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.49e-304 322.00 100.00% 100.00% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB:

US-10-079-111-1 (1-322) x ABX71612 (1-2372)

- 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20 à g
  - ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40 21

| qq            | 220                                                                             |                             |
|---------------|---------------------------------------------------------------------------------|-----------------------------|
| δλ            | 2y 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla              |                             |
| qu            | 280                                                                             |                             |
| δλ            | . 61                                                                            |                             |
| đ             | 040 TGTMGGCTGGGAGACTAAGTTTGGCCGGGAAGGACCAAGTTGAAACAGCCTTGAAAGCC                 |                             |
| λ<br>d        | 2y 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArgile              |                             |
| à             |                                                                                 | alLeuIleTrpLysValProVal 120 |
| QΩ            |                                                                                 |                             |
| ò             |                                                                                 | SpThrTrpThrAsnSerCysIle 140 |
| ΩQ            |                                                                                 |                             |
| & A           | 2y         141 ProGluilelleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160 |                             |
| ò             |                                                                                 | erProTyrSerThrileProAla 180 |
| qu            |                                                                                 |                             |
| δλ            |                                                                                 | leProArgArgLysLysLeuile 200 |
| Ob            |                                                                                 | TCCACGGAGAAAAATTGATT 759    |
| δ             |                                                                                 | orThrGluThrGluProPheVal 220 |
| qq            |                                                                                 | TACAGAAACTGAACCATTTGTT 819  |
| ò             |                                                                                 | 1eGlyGlyValProThrAlaLeu 240 |
| qq            |                                                                                 | redakadrerecekedeerera 879  |
| δ i           |                                                                                 | .yLeuGlyPheCysTyrValLys 260 |
| q             |                                                                                 | irctiggalitigciatgicaaa 939 |
| δλ            |                                                                                 | nGlnLysGluMetIleGluThr 280  |
| qq            |                                                                                 | GCAGAAGGAAATGATCGAAACC 999  |
| λŏ            |                                                                                 | OAsnGluGluSerLysLysThr 300  |
| qq            | 1                                                                               | TAATGAGGAATCAAAGAAAACT 105  |
| ð 1           |                                                                                 |                             |
| Q<br>O        | ī                                                                               | TACCGTGCGATGCCTGGAAGCT 111  |
| ò             |                                                                                 |                             |
| QΩ            | ਜ                                                                               |                             |
| RESUI<br>ACHO | 5944<br>ACH06                                                                   |                             |
| S S S         | ACH06944;                                                                       |                             |
| \$E\$         | 08-OCT-2003                                                                     |                             |
| E X           | Human secreted/transmem                                                         | cDNA.                       |
| KW            | Human; gene; ss; ab                                                             | cal disease; asthma;        |

```
gastrointestinal mucosa disorder; acute mucosal lesion, neuropathy; ALS; chronic mucosal lesion; abnormal keratinocyte differentiation; psoriasis; parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; uncontrolled cell growth, cancer; blood coagulation cascade; thrombosis; haemorrhage; endometrial bleeding; angiogenesis; wound healing; tumour; tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing.
hysterectomy; angiogenesis; coronary ischaemic condition; skin disease;
   97US-0063128P.
97US-0063327P.
97US-0063329P.
97US-0063541P.
97US-0063542P.
   9705 0063544P.
9705 0063549P.
9705 0063554P.
9705 0063354P.
9705 0063354P.
9705 0063724P.
9705 0063734P.
9705 0063734P.
9705 0063734P.
9705 0064215P.
9705 0064218P.
9705 0064248P.
9705 0064248P.
9705 0064248P.
9705 0064248P.
9705 0064248P.
   97US-0063045P.
97US-0063120P.
97US-0063121P.
97US-0063127P.
   970S-0059115P
970S-0059117P
970S-0059119P
970S-0059121P
970S-0059122P
970S-0059184P
   97US-0059263P.
97US-0059266P.
97US-0062125P.
  97US-0066466P.
   97US-0062285P.
  97US-0063486P.
97US-0062814P.
   97US-0066364P
  97US-0066770P
97US-0066772P
  97US-0066840P
97US-0069425P
  97US-0062816P.
   98US-0088026P
   98US-0099803P
   98US-0100262P
  10-JUL-2001; 2001US-00902903
   US2003044839-A1.
  Homo sapiens.
  31-OCT-1997;
31-OCT-1997;
03-NOV-1997;
   21-NOV-1997;
24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
   12-NOV-1997;
17-NOV-1997;
18-NOV-1997;
   1997;
   1997;
   06-MAR-2003.
  28-OCT-1997,
  1997;
   21-NOV-1997
  24-NOV-1997
24-NOV-1997
  25-NOV-1997
12-DEC-1997
  04-JUN-1998
  17-0CT-1997
17-0CT-1997
   21-OCT-1997
  24-0CT-1997
  24-OCT-1997
   24-OCT-1997
   28-OCT-1997
  28-OCT-1997
   17-SEP-1997
   18-SEP-1997
   24-OCT-1997
  OCT-1997
  27-0CT-1997
   28-OCT-1997
   28-OCT-1997
  17-SEP-1997
  17-SEP-1997
  29-OCT-1
29-OCT-1
   29-OCT-
  29-OCT-
   29-0CT-
```

98WO-US019330

```
The invention relates to an isolated PRO polypeptide. PRO317 is useful in disagnosing or treating abnormal bleeding involved in gynecological diseases e.g. to avoid or lessen the need for hysterectomy. PRO317 may also be useful as an agent that affects angiogenesis and PRO317 is useful and PRO317 polypeptides are useful for treating disorders conditions. PRO217 polypeptides are useful for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis). PRO3187 polypeptide is useful for treating Parkinson's disease, and disease, amyotrophic lateral sclerosis (ALS), neuropathies and disease related to uncontrolled cell growth, e.g. cancer. PRO219 polypeptides which serves as tumour specific antigens may be polypeptide which serves as tumour specific antigens may be polypeptide is useful as an antithrombotic agent with reduced risk for haemorhage as compared with heparin. PRO317 polypeptide is useful in the prolypeptide is useful in the maintening endometrial bleeding angiogenesis. PRO289 polypeptides and compared with heparin. PRO317 polypeptide is useful in the prolypeptide as compared with heparin. PRO317 polypeptide is useful in PRO314 polypeptides are useful for treating asthma, rheumatoid arthritis, portion have therapeutic applications in wound healing and tissue repair. PRO284 polypeptides are useful for treating asthma, rheumatoid arthritis, procriasis and multiple sclerosis. The polypeptide and its nucleic acid
   Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases.
  n ME, Goddard A;
Kljavin IJ;
  Ferrara N;
  Tumas D;
   Forg S, Gao W, C. .... Hillau ..., Grimaldi JC, Gurney AL, Hillau ...,
   snoyers L, Eaton DL,
Gerber H, Gerritsen
Irney AL, Hillan KJ,
  Botstein D, Desnoyers L,
   Claim 3; Fig 73; 478pp; English
   98US-0109304P.
98WO-US025108.
98US-0113296P.
99US-0143048P.
99US-0145698P.
  99WO-US028565.
99WO-US030095.
99WO-US030911.
99WO-US030999.
   2000WO-US000219.
2000WO-US003565.
  2000WO-US004414.
   30-MAR-2000; 2000WO-US008439.
   22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015264.
  2000WO-US020710.
2000WO-US023328.
  99US-0146222P.
  99WO-US020944.
   99WO-US028313.
99WO-US028301.
  99WO-US028564
  2000WO-US007377
  2000US-00665350
   99WO-US021547
  99WO-US023089
  Pan J, Pao
4, Wood WI;
   (GETH ) GENENTECH INC.
  WPI; 2003-492258/46.
P-PSDB; ABO47397.
   Ashkenazi A,
Filvaroff B,
Godowski PJ,
  Williams PM,
  02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
20-DEC-1999;
  22-FEB-2000;
24-FEB-2000;
   05-JAN-2000;
  11-FEB-2000;
   30-NOV-1999;
  28-JUL-1999
   666
  Mather JP,
   15-SEP-1
  13-SEP-1
   29-NOV-1
  05-0CT
```

```
AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
                                       LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
  AAAGTAGTAAAGGAGGAGGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAAAACT
  AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla
  GATAAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT
     cDNA encoding human secreted polypeptide PRO263
  Human; ss; gene; gene therapy; tumour; cancer
  ACA58812 standard; cDNA; 2372 BP
  98KR-00062142.
99WO-US005028.
99WS-0031033.
99WS-00380137.
99WS-00380138.
99WS-00380142.
99WS-00380142.
  2001US-00869599.
2001US-00908827.
2001US-00006867.
   2000WO-US015264.
2000US-00644848.
2000WO-US023328.
   2002US-00063616
  99US-00423844.
99WO-US031274.
   2000WO-US004341
   2000WO-US005601
  2000WO-US005841,
  2000WO-US007532.
   2000US-00664610
2000US-00665350
   2000WO-US030873
   2000WO-US032678
  2000WO-US034956.
   2001US-00816744.
  2000US-00709238
   2000US-00747259
  2001WO-US006520
   2001US-00854208.
2001US-00854280.
  2001US-00870574
  2001US-00874503
   (first entry)
   1125
   GluVal 322
  US2003013855-A1.
   GAAGTT
  14-NAY-1999;
25-AUG-1999;
25-AUG-1999;
25-AUG-1999;
15-SEP-1999;
18-OCT-1999;
18-OCT-1999;
18-PEC-1999;
18-PEC-1000;
201-MAR-2000;
21-MAR-2000;
22-MAY-2000;
   02-JUN-2000; 22-AUG-2000; 22-AUG-2000; 24-AUG-2000; 218-SEP-2000; 208-NOV-2000; 210-NOV-2000; 201-DEC-2000; 2
  29-JUN-2001;
18-JUL-2001;
06-DEC-2001;
   03-MAY-2002;
  30-DEC-1998;
08-MAR-1999;
14-MAY-1999;
   10-JUN-2003
  20-DEC-2000;
  16-JAN-2003
  1000
  1060
   321
  1120
   301
  ACA58812;
                                      281
   ACA5883
  g
   g
  8
  à
  ద
   à
are useful for tissue typing. PRO antibodies are useful for immunohistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents CDNA encoding a human secreted/transmembrane
  219
  279
   339
   399
   100
  459
   519
   140
   160
   120
  579
  639
   180
  879
  669
   200
  759
  220
  819
  240
   LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
   939
  40
  9
   261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
   80
  MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu
  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
   GTCCAAGGCTCTTTGCGTGCAGAGGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
   IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
   CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
   SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
   SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
   ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
  AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGTTGGATTCGTGGTCATCTTAGGATT
   GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal
   ProGluilelleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
  CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCCACGGGGAAAAATTGATT
  580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA
  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuile
   GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyClyValProThrAlaLeu
  CTAGTGCTTGCTCCTCTTTTGGTGCTGCTGGTCTTGGATTTTGCTATGTCAAA
  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
   0 U; 0 Other;
  2372
322
0
0
0
   Length:
Matches:
Conservative:
Mismatches:
Indels:
   489 G; 638 T;
  Gaps:
   (1-2372)
  ς;
  US-10-079-111-1 (1-322) x ACH06944
   1.49e-304
322.00
100.00%
100.00%
  Sequence 2372 BP; 721 A; 524
  Percent Similarity:
Best Local Similarity:
  PRO polypeptide
  gnment Scores:
   160
   21
   220
  41
  280
  340
   460
  61
  81
   400
  101
   640
   121
   141
   241
   161
   181
   700
   201
   760
  221
  820
   Query Match:
DB:
  Score:
 5555555x8
   à
   g
   g
   gg
  a
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   g
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   요
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```

Goddard A, Godowski PJ; Wood WI;

Gerritsen ME, Watanabe CK,

```
New isolated antibody specifically binding a PRO polypeptide, useful for the preparation of a medicament for treating disorders with the aberrant expression or activity of the PRO polypeptide, such as tumor conditions and cancer.
             Filvaroff E,
C, Gurney AL,
(GETH ) GENENTECH INC.
                                     WPI; 2003-330485/31.
P-PSDB; ABU71508.
               Eaton DL, Fi
Grimaldi JC,
```

The invention relates to an antibody that binds to a polypeptide with a fully defined sequence given in the specification. The methods and compositions (containing antibodies that specifically bind a PRO compositions (containing antibodies that specifically bind a PRO compositions (containing antibodies that specifically bind a PRO colypeptide) of the present invention are useful for the preparation of a medicament for the treatment of disorders associated with the aberrant can can cancer. They can also be used to generate transgenic or knockout animals useful in the development and screening of therapeutically useful reagents. The PRO polypeptides and encoding nucleic acids can be used as molecular weight markers for protein electrophoresis, chromosome identification and tissue typing. The PRO polypeptides are useful to induce angiogenesis e.g wound healing; in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis, diabetes; hyperinaulinaemia and hypoinsulinaemia. The arthritis diabetes; hyperinaulinaemia and hypoinsulinaemia. The immunoprecipitation assays. The present sequence represents a cDNA encoding a PRO polypeptide of the invention Example 4; Page 69-70; 406pp; English.

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

|                                                                                                  |               | 20                         | 219                                                           | 0.4                    | 279                                                          | 09        | 339                                                          | 80                            | 399                                                                | 100                   | 459                                          | 120                      | 519                                               | 140                                   | 579                              |
|--------------------------------------------------------------------------------------------------|---------------|----------------------------|---------------------------------------------------------------|------------------------|--------------------------------------------------------------|-----------|--------------------------------------------------------------|-------------------------------|--------------------------------------------------------------------|-----------------------|----------------------------------------------|--------------------------|---------------------------------------------------|---------------------------------------|----------------------------------|
|                                                                                                  |               | n=                         |                                                               | G15                    |                                                              | ส —       |                                                              |                               |                                                                    | υ                     |                                              |                          |                                                   | υ                                     |                                  |
|                                                                                                  |               | eul.                       | TCC                                                           | letg<br> -             | -13<br>-13<br>-13<br>-13                                     | Au I      | 3AGG                                                         | ysA<br>                       | AAGCT                                                              | rgi                   | CTAGGATT                                     | Prov                     | CCAG                                              | (3ys1                                 | -05<br>-05                       |
|                                                                                                  |               | rpThrThrArgLeuL            | 9000                                                          | 1] eV                  | ALL                                                          | Lyse      | AAGC                                                         | LeuI                          | TTG                                                                | Ser                   |                                              | ysvalProval              | GTTC                                              | Ser(                                  | Crccrccarr                       |
|                                                                                                  |               | Thri                       | ACG.                                                          | Arg                    | AGA                                                          | Ala]      | GCT                                                          | A1a)                          | CAGCCT                                                             | 11e                   | ATC.                                         | Lys.                     | AAG                                               | Asn                                   |                                  |
|                                                                                                  |               | Thr                        | ACC                                                           | 7.7.<br>               | ATGC-                                                        | 191<br>   | AGAA                                                         | Thr                           | AACA                                                               | [Va]                  | 3GTC                                         | leTrpI                   | 1100                                              | oThr                                  | TGGACTAA                         |
| 2372<br>322<br>0<br>0<br>0                                                                       |               | eTrp                       | 11.0                                                          | eGlnValSerCysArgIleMet | 3TC                                                          | eThr      | CAC                                                          | ysAspGlnValGluThrAlaLeuLysAla | CCAAGTTGAAA                                                        | yPheValValileSerArgil | CGTC                                         | ii.                      | GAT                                               | rr-                                   | 11<br>17<br>17<br>17<br>17<br>17 |
| 2,0000                                                                                           |               | erIl                       | CAT                                                           | nVa<br>                | -E                                                           | nPh<br>   | LL                                                           | nVa<br>                       | AGT                                                                | YPh<br>               | ATT                                          | ll Le                    | -00<br>-01                                        | dTq:                                  | TAC                              |
| <br>                                                                                             |               | rse                        | TIC                                                           | -eg                    | -00                                                          | euAs      | GA                                                           | pg:                           | - CC                                                               | yAspG]                | ATG                                          | 1yVa                     | 316                                               | erAs                                  | CTGA                             |
| Length:<br>Matches:<br>Conservative<br>Mismatches:<br>Indels:<br>Gaps:                           |               | SPheSerLeuValLeuLeuLeuThrS | TCAC                                                          | euArgAlaGluGluLeuSerIl | CCA                                                          | Jul.      | AGC                                                          | YSA                           | ccggcaagga                                                         |                       | TTGAAACTTGCAGCTATGGCTTGGAGATGGATTCGTGGTCATCT | VLysAsnGlyValGlyValLeuIl | CCAAGTGGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG | ysTyrasnSerSeraspThrTrpThrasnSerCysI1 | TCAT                             |
| Length:<br>Matches<br>Conserv<br>Mismatcl<br>Indels:<br>Gaps:                                    | _             | euL<br>                    | TIC                                                           | ens                    | TI                                                           | ThG<br> - | AGC                                                          | 31 y L                        | - 4<br>- 2<br>- 3<br>- 4                                           | rpvalg                | TTG                                          | 31yV                     | -00<br>-00<br>-00                                 | AsnS                                  | AACT                             |
| Lengt<br>Match<br>Conse<br>Misma<br>Indel<br>Gaps:                                               | (1-2372)      | leuI                       | TIGG                                                          | 12.5                   | 3AGC                                                         | AsnG      | ACC<br>ACC                                                   | 41aG                          | 3000<br>3000                                                       | Trp                   | 199-                                         | Asn(                     | AATC                                              | Tyr!                                  | TAC                              |
|                                                                                                  | (1-3          | Vall                       | GTG                                                           | 31n(                   | GAAA                                                         | Alaj      | -00<br>-00<br>-00                                            | Leu                           | 111G                                                               | G13                   | -0<br>-0<br>-0                               | Lys                      | -A-                                               | Cys<br>                               | TGT                              |
| 4"                                                                                               | 17            | Leu                        | CTG                                                           | Ala                    | GCA<br>GCA                                                   | Lys       | AAG                                                          | Ser                           | AGT                                                                | Y.                    | TAT                                          | ysgly                    | - 100-<br>- 100-                                  | TYT8                                  | CTAT                             |
| 49e-304<br>2.00<br>0.00%<br>0.00%<br>0.00%                                                       | ACA58812      | Ser                        | SAGC                                                          | Arg                    | 3001                                                         | rLys<br>  | AAA                                                          | The                           | ACTA                                                               | sser'                 | CAG                                          | SCys                     | GTG.                                              | aAla                                  | ₽GC(                             |
| 1.49e-30<br>322.00<br>100.00%<br>100.00%<br>7                                                    |               | SPh(                       | CTT                                                           | erLe                   | TTT                                                          | 13e       | GAG                                                          | , LG                          | -9<br>-9<br>-9                                                     | -::                   | TIG                                          | ory<br>-                 | CAA                                               | leA]                                  | TGC                              |
|                                                                                                  | ×             | -7:                        | GTG                                                           | yse                    | CTC                                                          | uVa<br>   | TGT                                                          | uLe                           | CTGCTGGGACTAAGTTTGG                                                | LuTh                  | AAA<br>AAA                                   | SnPr                     | ACCC                                              | InPh                                  | AGTI                             |
| ity:                                                                                             | (1-322)       | LaArg(                     | CCAC                                                          | GlnGlyS                | AAGG                                                         | hrle      | -0-<br>-0-                                                   | rgi-                          | -00<br>-00<br>-00<br>-00<br>-00<br>-00<br>-00<br>-00<br>-00<br>-00 | heG]                  | TTG                                          | roA                      | - <b>F</b>                                        | rgg<br> -                             | GAC                              |
| s:<br>ity<br>lar:                                                                                |               | MetAl                      | AFGGCCAGGTGCTTCAGCCTGGTGGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG | ValG                   | GTCCAAGGCTCTTTGCGTGCAGAGAGAGTTTCCATCCAGGTGTCATGCAGAATTATGGGG |           | ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC | CysArgLeuLeuGlyLeuSerLeuAlaGl | TGTAGG                                                             | SerPheGluThr          | AGCT                                         | SerProAsnProLy           | AGCCCAAACC                                        | SerArgGlnPheAlaAlaTy                  | AGCCGACAGITIG                    |
| t Scores: .: Similarity al Similar                                                               | 1-1           | Ε-Ξ                        | 160 A                                                         | 21 V                   | 220 G                                                        | 41 T      | 280 A                                                        | 61 0                          | 340 T                                                              | 81 8                  | 4004                                         | 101                      | 460 7                                             | 121                                   | 520 #                            |
| hent Sc<br>No.:<br>ht Simi<br>hocal S<br>Match:                                                  | 9-11          |                            | 16                                                            | N                      | 22                                                           | 4         | 28                                                           | v                             | 34                                                                 | w                     | 4                                            | Ä                        | 4                                                 | H                                     | 2                                |
| ment<br>No<br>:<br>:<br>nt (<br>Lock                                                             | -07           |                            |                                                               |                        |                                                              |           |                                                              |                               |                                                                    |                       |                                              |                          |                                                   |                                       |                                  |
| Alignment Scores: Pred. No.: Score: Scoret Scoret Similarity: Best Local Similarity Query Match: | US-10-079-111 |                            | _                                                             |                        | 0                                                            | _         | 0                                                            | _                             | 0                                                                  | >-                    | ۵                                            | >-                       | ۵                                                 | >-                                    | qq                               |
| Pre-                                                                                             | US            | δ                          | qq                                                            | δ                      | qq                                                           | δδ        | qq                                                           | ò                             | qq                                                                 | ò                     | qa                                           | ò                        | qq                                                | δλ                                    | Д                                |

80

160

180 669 200 759 220 819 240 879

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1060 GATAAAAACCCAGAAGAGTCCAAGAGCAAAACTACCGTGCGATGCCTGGGAAGCT 1119
  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
  transmembrane protein; rectal;
cancer; cytostatic;
   CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
                             340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
  SerPheGluThrCysSerTyrGlyTrpValGlyABpGlyPheValValIleSerArgIle
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   460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
  GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
  AGCCGACAGTITGCAGCCTATTGTTACAACTCATCTGGATACTTGGACTAACTCGTGCATT
  ProGluileileThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
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   ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle
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   CysvalThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
   GluAsniysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
   820 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
   LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
  261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
   AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
   Human, PRO polypeptide; secreted protein, lung; stomach; oesophageal; skin; tumour;
   cDNA encoding human PRO polypeptide #3
  ACA91252 standard; cDNA; 2372 BP
  (first entry)
  gene therapy; gene; ss
  1125
   GluVal 322
  GAAGIT
  14-JUL-2003
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  121
   520
  141
   580
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  The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of a condition responsive to anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ACA63986-ACA64069 represent coll culture or natural sources. polypeptides of the invention
   279
   as
   40
   IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
  \ensuremath{\mathsf{i}} isolated secreted transmembrane polypeptide designated PRO, useful therapeutic agent.
   MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu
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  Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
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322
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Gaps:
   Wood WI;
  Gerritsen ME,
Watanabe CK,
   x ACA63988 (1-2372)
   Disclosure, Fig 5; 236pp, English.
                         21. MAR. 2000; 2000MC-US0U3591.
22. MAY-2000; 2000MC-US0U3591.
22. MAY-2000; 2000MC-US014042.
22. MG-2000; 2000MC-US01564.
24. MG-2000; 2000MG-US023328.
18. SEP-2000; 2000WG-US03328.
18. SEP-2000; 2000WG-US03328.
10. NOV-2000; 2000WG-US033873.
01. DEC-2000; 2000WG-US033873.
01. DEC-2000; 2000WG-US034956.
20. DEC-2000; 2000WG-US034956.
20. DEC-2000; 2000WG-US034956.
22. MAR-2001; 2001WG-US034956.
22. MAR-2001; 2001WG-US034956.
23. MAR-2001; 2001WG-US034956.
24. MAR-2001; 2001WG-US054208.
30. MAR-2001; 2001WG-US057480.
30. MAR-2001; 2001WG-US057780.
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100.00%
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  2001US-00874503.
2001US-00869599.
2001US-00908827.
   Eaton DL, Filvaroff E,
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  (GETH ) GENENTECH INC.
   WPI; 2003-328612/04.
  US-10-079-111-1 (1-322)
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01-MAR-2000;
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280

Length:
Matches:
Conservative:
Mismatches:

1.49e-304 322.00 100.00% 100.00%

Percent Similarity: Best Local Similarity: Query Match:

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Indels: Gaps:

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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptide and polynucleotide sequences are useful for the diagnosis, prevention and treatment of rectal, lung, stomach, coscophageal or skin tumours, and/or cancers. The PRO polypeptides are also useful as molecular weight markers. The PRO polynucleotide sequences are useful for chromosome identification, hybridisation probes, and for sereening libraries of human cDNA, genomic DNA or mRNA. They may also be used in gene therapy, particularly for replacing a defective gene. ACA91250-ACA91333 represent cDNA sequences encoding the human PRO polypeptides of the invention
   New isolated, secreted and transmembrane PRO polypeptide, useful for the diagnosis, prevention and treatment of rectal, lung, stomach, esophageal or skin cancers.
   Godowski PJ;
  Goddard A,
Wood WI;
   Gerritsen ME,
Watanabe CK,
  Disclosure; Fig 5; 235pp; English.
   24-AUG-2000; 2000W0-US023328.
18-SEP-2000; 2000W0-US023328.
18-SEP-2000; 2000WS-00064610.
18-SEP-2000; 2000WS-00065350.
08-NOV-2000; 2000WS-00709238.
10-NOV-2000; 2000WS-00709238.
20-DEC-2000; 2000WS-00747259.
20-DEC-2000; 2000WS-00747259.
28-FEB-2001; 2001WS-00816744.
10-MAY-2001; 2001US-00854208.
   98KR-00062142.
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2000WO-US005841.
  2000WO-US007532
  2000WO-US014042.
2000WO-US015264.
  2000US-00644848
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   2001US-00874503
   2001US-00869599
2001US-00908827
  2002US-00063569
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  (GETH ) GENENTECH INC.
   2003-401699/38
   WPI; 2003-401699,
P-PSDB; ABU90962
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22-MAY-2000;
02-JUN-2000;
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  14-MAY-1999;
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25-AUG-1999;
25-AUG-1999;
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  22-AUG-2000;
  02-MAY-2002;
  18-FEB-2000;
   12-NOV-1999;
30-DEC-1999;
                         23-JAN-2003
   Eaton
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Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

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  TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
   GluAsniysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu
  GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTG
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  CTAGTGCTTGCTCTCTTCTTTGGTGCTGCTGCTGTTTTGGATTTTGCTATGTCAAA
   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
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  GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
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  940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
  AAAGTAGTAAAAGGAGGAGGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
   GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGGTGTCATGCAGAATTATGGGG
   IleThrLeuValSerIysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
   TGTAGGCTGCTGGGCTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
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   CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                      MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu
                                 160 ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG
   CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
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  (1-2372)
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  New isolated antibody specifically binding a PRO polypeptide, useful for
the preparation of a medicament for treating disorders with the aberrant
expression or activity of the PRO polypeptide, such as tumor conditions
   Godowski PJ;
  Human; ss; tumour; cancer; gene therapy; tissue typing; gene.
  Human secreted/transmembrane polypeptide PRO263 cDNA.
  Goddard A,
Wood WI;
   Gerritsen ME,
Watanabe CK,
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  CDNA; 2372
  2000US-00644848.
2000WO-US023328.
2000US-00664610.
2000US-00665350.
2000US-00709238.
   99WO-US005028.
99US-00311832.
99WO-US010733.
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2001US-00854280.
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  2000WO-US005841
2000WO-US007532
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  (GETH ) GENENTECH INC
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C, Gurney
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321 GluVal 322
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18-OCT-1999;
   MAY-2001;
   11-SEP-2003
   09-JAN-2003
   12-NOV-1999
   ACD45151;
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The invention relates to an antibody that binds to a secreted and transmembrane PRO polypeptide. The methods and compositions of the present invention are useful for the preparation of a medicament for the treatment of disorders associated with the aberrant expression or activity of the PRO polypeptide, such as tumour conditions and cancer. They can also be used to generate transgenic or knockout animals useful in the development and screening of therapeutically useful reagents. The PRO polypeptides and encoding nucleic acids can be used as molecular weight markers for protein electrophoresis, chromosome identification and tissue typing. The antibodies may be used in various diagnostic, competitive binding and/or imminoprecipitation assays. The present
  219
  120
  339
   519
  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCyslle 140
  180
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   MetAlaArgCysPheSerLeuValLeuLeuTeuThrSerIleTrpThrThrArgLeuLeu 20
   40
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  80
  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
  639
   CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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   280 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
   CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
  460 AGCCCAAAACCCCAAGTGTGGGGAAAATGGGGTGTGTCTTTTTTTGGAAGGTTCCAGTG
   GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
   CCTACTACTACTCCTCCTGCTCCAGCTTCCATTCCACGGAGAAAAATTGATT
   SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
  520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
   GAATTTATIGICAGIGACAGIACCTACTCGGIGGCAICCCCTIACTCTACAGIATACCTGCC
   ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle
  sequence represents a secreted and transmembrane PRO polypeptide
  Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
   2372
322
0
0
0
0
   Conservative:
Mismatches:
Indels:
  Length:
Matches:
   US-10-079-111-1 (1-322) x ACD45151 (1-2372)
Dislcosure; Fig 5; 223pp; English.
  1.49e - 304
  322.00
100.00%
100.00%
   160
  g
```

```
New secreted and transmembrane PRO polypeptides (e.g. PRO533 or PRO245) and genes encoding them, useful for detecting or treating e.g. hyperplasia, endometriosis, cancers, ischemia, coronary arterial disease or inflammations.
  Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; an J, Paoni NP, Roy MA, Stewart TA, Tumas D;
   9705-0065186F
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   2000WO-US005841.
   2000WO-US007377
2000WO-US008439
  98WO-US019177.
   98WO-US019330.
  98WO-US025108
99WO-US020594
  99WO-US021090
  99WO-US021547
   99WO-US023089
   99WO-US028214
  99WO-US028313
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   99WO-US028565
   2000WO-US023328
  2000US-00665350
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   (GETH ) GENENTECH INC
   WPI; 2003-288105/28.
P-PSDB; ABU64534.
   Pan J,
  Ashkenazi A, B
Filvaroff E, F
Godowski PJ, G
  05-JAN-2000; 2
11-FEB-2000; 22-FEB-2000; 24-FEB-2000; 20-MAR-2000; 30-MAR-2000; 30-MAR-2000; 20-MAR-2000; 20-
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24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
10-SEP-1998;
  15-SEP-1999;
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29-NOV-1999;
  22-MAY-2000;
02-JUN-2000;
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  28-OCT-1997;
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29-OCT-1997;
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   17-SEP-1998;
   01-DEC-1998;
   1999;
  14-SEP-1998;
  12-NOV-1997
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   13-SEP-1
15-SEP-1
  30-NOV-
  16-SEP-
  08-SEP-
   AAAGTAGTAAAGGAGGAGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT 1059
   260
   300
   320
                                  879
  939
   280
  999
  Human; gene; ss; PRO; secreted, transmembrane; pharmaceutical; diagnostic; biosensor; bioreactor; therapeutic; hyperplasia; endometriosis, cancer; umour; ischaemia; ocnomary arterial disease; polycystic kidney disease; rend failure; inflammatory response; asthma; rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy; cytostatic; gynecological; cardiant; nephrotropic; hepatotropic;
                     GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
   LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
   CTAGTGCTTGCTCTCCTTCTTTGGTGCTGCTGGTCTTGGATTTTGCTATGTCAAA
   AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATGAACC
   AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
      GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
   ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
  Human secreted/transmembrane protein cDNA, #38
   BP.
   97US - 0059113P .
97US - 0059115P .
97US - 0059117P .
97US - 0059121P .
97US - 0059124P .
97US - 0059268P .
97US - 0062125P .
97US - 0062125P .
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97US - 0062287P .
  97US-0062814P.
97US-0062816P.
97US-0063045P.
97US-0063120P.
  97US-0063121P.
97US-0063127P.
97US-0063128P.
97US-0063327P.
97US-0063329P.
97US-0063329P.
   ABX96181 standard; cDNA; 2372
   (first entry)
   GAAGTT 1125
  GluVal 322
  antiinflammatory
   US2002160374-A1
   17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
18-SEP-1997;
11-OCT-1997;
17-OCT-1997;
17-OCT-1997;
18-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
   12-JUL-2001;
   13-MAY-2003
  31-OCT-2002
   27-OCT-1997
27-OCT-1997
  1000
   1120
                                     820
  241
  880
   261
  940
   281
  1060
   321
  ABX96181;
   301
      221
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  RESULT 25
  ABX9618:
   Db
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97US-0062814P.
97US-0063145P.
97US-0063121P.
97US-0063121P.
97US-0063127P.
97US-0063127P.
97US-0063327P.
97US-0063328P.
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  (first entry)
  1125
   GluVal 322
   US2003023054-A1.
  GAAGTT
  Homo sapiens.
   29-MAY-2003
   16-JUL-2001;
   15-OCT-1997;
17-OCT-1997;
17-OCT-1997;
21-OCT-1997;
   27-OCT-1997;
28-OCT-1997;
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   17-SEP-1997;
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  30-JAN-2003
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   17-SEP-1997
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  17-SEP-1997
   18-SEP-1997;
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24-OCT-1997;
   24-0CT-1997;
   24-OCT-1997
   880
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   321
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                                The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polymucleotides are also useful as pharmaceuticals, diagnostics, polymucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. hyperplasia, endometriosis, cancers (e.g. those involving solid tumours), ischaemia, coronary arterial disease, polycystic kidney disease, chronic or acute arthritis, psoriasis or multiple sclerosis) in mammals. The PRO genes may also be used in gene therapy, particularly for replacing a defective encoding, the primers amplifying and the probes detecting the PRO polynucleotides of the invention
  279
   339
   399
   519
   SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
  100
   459
  120
  819
   ProGluilelleThrThrLysAspProilePheAsnThrGlnThrAlaThrGlnThrThr 160
  639
   180
  669
   40
   9
  80
   MetAlaArgCysPheSerLeuValleuLeuLeuThrSerIleTrpThrThrArgLeuLeu
  ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArg1leWetGly
   GTCCAAGGCTCTTTGCGTGCAGGAGGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
   ATCACCCTTGTGAGCAAAAAGGCAAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
   TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
  SerProAsnProLysGysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal
  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
   460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
   GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThr1leProAla
   AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT
  520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGGATACTTGGACTAACTCGTGCATT
  ccaganatratcaccaacaagarccarararcaacacrcaaacrgcaacacaaaaaaa
   ProThrThrThrProProAlaProAlaSerThrSerileProArgArgLysLeuile
   CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
  Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
   2372
322
0
0
0
   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
  US-10-079-111-1 (1-322) x ABX96181 (1-2372)
Claim 2; Fig 73; 477pp; English
   1.49e-304
   322.00
100.00%
100.00%
100.00%
  Percent Similarity:
Best Local Similarity:
  Alignment Scores:
   21
   220
  41
   340
   400
  61
  81
  101
   141
   161
   181
   260
   Query Match:
DB:
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No..
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16-DEC-1999; 99W0-US030095.

20-DEC-1999; 99W0-US030091.

20-DEC-1999; 99W0-US030911.

05-JAN-2000; 2000W0-US000219.

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  2000WO-US015264.
   296P.
   99US-0143048P.
   99WO-US028565.
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07-JUL-1999;
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08-SEP-1999;
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17-SEP-1998;
17-SEP-1998;
  13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
29-NOV-1999;
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   03-NOV-1997;
07-NOV-1997;
  10-SEP-1998
   14-SEP-1998
   14-SEP-1998;
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```

Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; (GETH ) GENENTECH INC Ashkenazi A, Filvaroff E, Godowski PJ,

the invertion traters to sixty one nuction actioning from propertides (secreted and transmembrane). The polymucleotide is useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polymucleotide may also be used in preparing PRO competitions by recombinant techniques, and in generating either competitions by recombinant techniques, and in generating properties by recombinant techniques, and in generating either competition of the antibody is used in preparing a medicament for polymeptide or the antibody is used in preparing a medicament for competing a condition responsive to the polymeptide or antibody, such as mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g. psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease constraints at disease and Parkinson's disease, Usher syndrome, atrophia areata, angiogenesis, inflammatory disease e.g asthma and crhemmatoid arthritis, ischaemia, and in various disease e.g asthma and crhemmatoid arthritis, ischaemia, and in various disease e.g asthma and crhemmatoid extremesents an CDNA which encodes a PRO polypeptide Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in treating cancer and Alzheimer's disease. Ä invention relates to sixty one nucleic acids encoding PRO Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other; Tumas Stewart TA, Roy MA, Example 33; Fig 73; 481pp; English NF, Paoni Pan J, Pā Wood WI; WPI; 2003-331485/31. P-PSDB; ABU67380 Mather JP, P Williams PM, 

2372 322 0 0 0 Conservative: Mismatches: Indels: Length: Matches: Gaps: (1-2372)US-10-079-111-1 (1-322) x ACA05502 1.49e-304 322.00 100.00% 100.00% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB: Pred. No.:

MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArglleMetGly 220 grccaaggcrcrrrgcgrgcagaagagcrrrccarccaggrgrcargcagarrrarggg 11eThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 280 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 41 Н 61

> 엄 ð Op ò g ò g à d à d à 8

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219

279

40

339

80

9

SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle AGCCGACAGITIGGAGCCIATIGITACAACTCATCIGATACTIGGACTAACTCGTGCATT 520 121

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US-10-079-111-1 (1-322) x ACA93699 (1-2372)
   Eaton
     ò
   1059
  200
   240
                    669
   759
   220
  879
  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
  280
   320
  939
  LysvalvalLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
  Human; ss; gene; PRO; secreted protein; transmembrane protein; cytostatic; vulnerary; osteopathic; antiarthritic; antirheumatic; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour necrosis factor; pericyte cell proliferation; TNF-alpha; proteoglycans release, cartilage; cancer; wound healing; cartilage defect; osteoarthritis; rheumatoid arthritis.
GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThr1leProAla
          GAATITATIGICAGIGACAGTACCIACIACHOOGAATCCCCTTACICTACAATACCIGCC
   GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTG
                                 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuile
  cradiderridereteretriretrindereereereereerengearringerandraa
   261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
  AAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
   301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
  Human cDNA encoding secreted/transmembrane protein PR0263.
  BP.
   ACA93699 standard; cDNA; 2372
  99US-00380137.
99US-00380138.
99US-00380139.
99US-00397342.
99US-00403297.
99US-00403297.
   99WO-US005028.
99WS-00311832.
99WS-US010733.
  2002US-00063553
   (first entry)
  1120 GAAGTT 1125
   GluVal 322
   US2003045684-A1,
  18-OCT-1999;
12-NOV-1999;
30-DEC-1999;
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   08-MAR-1999;
14-MAY-1999;
14-MAY-1999;
25-AUG-1999;
25-AUG-1999;
  02-MAY-2002;
  17-JUL-2003
   06-MAR-2003.
  25-AUG-1999;
  30-DEC-1998,
  15-SEP-1999
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   281
  1000
  1060
   321
 191
                 640
   200
  201
   160
  221
   820
   241
   880
  ACA93699;
à
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The invention relates to a new isolated PRO994 polypeptide comprises an amino acid sequence appearing as ABU92499, PRO994 lacking its associated signal peptide, the extracellular domain of PRO994, the extracellular domain of PRO994, the extracellular domain of PRO994, the extracellular contains of the contains of the children in a secondary of the contains of the contains and coded by the full-length coding sequence of the cDNA ATCC 203018. Also included is a chimaeric molecule comprising the PRO999 polypeptide fused to a heterologous amino acid sequence. The PRO polypeptide is useful in parmaceuticals, diagnostics, biosensors or bioreactors. It is particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF) alpha from human blood, for stimulating the proliferation of pericyte cells, or stimulating the release of proteoglycans from cartilage. The polypeptide may be employed for a variety of therapeutic purposes, e.g. for treating cancer, wound healing, cartilage defects, osteoarthritis, rheumatoid arthritis. Also disclosed are the cDNA encoding PRO994, 83 other PRO polypeptides and their encoding cDNAs. The present sequence
   New PRO994 polypeptide, useful for detecting tumors, or for stimulating Tumor Necrosis Factor alpha, or pericyte proliferation, especially for treating cancer, cartilage defects, osteoarthritis and rheumatoid arthritis in mammal.
  Godowski PJ;
   BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
   2372
322
0
0
0
   Goddard A,
Wood WI;
  Length:
Matches:
Conservative:
Mismatches:
  Indels:
   Gerritsen ME,
Watanabe CK,
   Disclosure; Fig 5; 235pp; English.
   20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001WO-US036520.
22-MAR-2001; 2001US-00816744.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
30-MAY-2001; 2001US-00870574.
01-JUN-2001; 2001US-00870574.
   2000WO-US015264.
2000US-00644848.
  2000WO-US023328.
2000US-00664610.
2000US-00665350.
   10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000US-00747259.
   2000WO-US014042
  2000US-00709238
  2001US-00869599
2001US-00908827
  18-JUL-2001; 2001US-00908827
06-DEC-2001; 2001US-00006867
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322.00
100.00%
100.00%
   Gurney AL,
  Filvaroff E,
   (GETH ) GENENTECH INC.
  WPI; 2003-392892/37.
   Best Local Similarity:
Query Match:
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02-MAR-2000; 2
22-MAY-2000; 2
02-MUN-2000; 2
22-AUG-2000; 2
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118-SEP-2000; 2
08-NOV-2000; 2
  Percent Similarity:
   Grimaldi JC,
   Sequence 2372
   29-JUN-2001;
   Alignment Scores:
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1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

```
25-AUG-2003
   240
   260
  939
   280
   999
   140
  200
   220
  819
   879
  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
  AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
  519
   579
   ProGlullelleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr 160
  639
  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
   669
   759
            219
   279
  339
   399
   SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
  400 AGCITIGAAACIIGCAGCIAIGGCIGGGIIGGAGAIGGAIICGIGGICAICICAGGAII 459
  120
  80
                                   40
   9
   SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
   GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
   LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
   AGCCCAAACCCCAAGTGTGGGAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
  520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
   ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
   CCTACTACTACTCCTCCTCCTCCTCCTTCTATTCCACGGGAAAAAATGATT
  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
   TGTGTCACAGAAACTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
   GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTG
  craerecriecreretretraderecrecedenderecresaritrecraretrade
   ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
   GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACATACTCTGCC
GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
   IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
   280 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
  TGTAGGCTGCTGGGAAAGTTTGGCCGCAAGGACCAAGTTGAAAACAGCCTTGAAAAGCT
  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeu1leTrpLysValProVal
                                    ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
   standard; cDNA; 2372
  GAAGTT 1125
   GluVal 322
  880
   940
  1000
  1060
  1120
   201
  260
  321
  ACD20169
   41
  340
  460
  640
   181
   700
   820
   241
   261
   281
  301
             160
                                    21
  220
  61
   81
  101
   141
   580
   161
  221
  121
  RESULT 28
   ACD20169
ID ACD2
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AC ACD2
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ACD20169

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Human; ss; gene; gene therapy; tumour; tissue typing; obesity; diabetes; hypoinsulianeamia: hyperinsulianeamia: hyperinsuliane
                                    Human secreted / transmembrane polypeptide PRO263 cDNA.
   9705-0059113P

9705-0059113P

9705-0059115P

9705-0059121P

9705-0059121P

9705-0059124P

9705-0059263P

9705-0062814P

9705-0062814P

9705-0062814P

9705-0063121P

9705-006312P

9705-006314P

9705-006314P

9705-006314P

9705-006314P

9705-006314P

9705-006314P

9705-006314P

9705-006631P

9705-006631P

9705-006631P

9705-006631P

9705-006631P

9705-006631P
   98WO-US018824
98US-0100262P
   2001US-00904859
(first entry)
   US2003036060-A1
   10-SEP-1998;
10-SEP-1998;
14-SEP-1998;
   12-JUL-2001;
   17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
   18-SEP-1997

18-SEP-1997

17-OCT-1997

24-OCT-1997

24-OCT-1997

24-OCT-1997

24-OCT-1997

24-OCT-1997

24-OCT-1997

24-OCT-1997

28-OCT-1997

28-OCT-1997

28-OCT-1997

28-OCT-1997

29-OCT-1997

21-OCT-1997

21-OCT-1997

21-OCT-1997

21-OCT-1997

21-OCT-1997

21-OCT-1997

21-OCT-1997
  03-NOV-1997;
07-NOV-1997;
12-NOV-1997;
  Homo sapiens
  . NOV-1997;
  17-SEP-1997
  NOV-1997
   NOV-1997
   NOV-1997
  NOV-1997
  NOV-1997
   NOV-1997
   NOV-1997
  DEC-1997
   17-NOV-1997
  20-FEB-2003
  -SEP-1997
   arthritis.
```

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2000WO-US004414.
2000WO-US00504.
2000WO-US005841.
2000WO-US007377.
2000WO-US00439.
2000WO-US014042.
2000WO-US014042.
2000WO-US01264.
   99WO-US028214.
99WO-US028313.
99WO-US028301.
  99WO-US028564.
99WO-US028565.
99WO-US030095.
                        98US-0104080P.
98US-0109304P.
98WO-US025108.
   99US-0145698P.
99US-0146222P.
99WO-US020594.
            98US-0100858P
98WO-US019437
  98US-0113296P
  99WO-US030911.
   99WO-US020944
  99WO-US021090
   99WO-US021547
   99WO-US023089
   99WO-US030999
  2000WO-US000219
  2000WO-US003565
  2000US-00665350
                             20-NOV-1998;
01-DEC-1998;
22-DEC-1998;
07-JUL-1999;
26-JUL-1999;
28-JUL-1999;
  02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
  22-FEB-2000;
   02-JUN-2000;
   20-MAR-2000;
30-MAR-2000;
                 17-SEP-1998;
13-OCT-1998;
   -JUL-1999;
   11-FEB-2000;
   24-FEB-2000;
   02-MAR-2000;
   22-MAY-2000;
  24-AUG-2000;
  18-SEP-2000;
  05-JAN-2000;
  05-OCT-1999;
  DEC-1999;
   13-SEP-1999;
15-SEP-1999;
  30-NOV-1999;
   20-DEC-1999
```

## (GETH ) GENENTECH INC.

Desnoyers L, Eaton DL, Ferrara N; W, Gerber H, Gerritsen ME, Goddard A; Gurney AL, Hillan KJ, Kljavin IJ; NF, Roy MA, Stewart TA, Tumas D; Ashkenazi A, Botstein D, Desr Filvaroff E, Fong S, Gao W, Godowski PJ, Grimaldi JC, Gu: Mather JP, Pan J, Paoni NF, Godowski PJ, Grimaldi Mather JP, Pan J, Pa Williams PM, Wood WI;

## WPI; 2003-417923/39. P-PSDB; ABO14900.

Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.

Claim 2; Fig 73; 469pp; English.

The invention relates to an isolated, secreted and transmembrane polypeptide, termed PRO polypeptide. The polypeptide is useful for dentifying agonists or antagonists of the polypeptide, for proparing variants of the polypeptide, as molecular weight markers for proteins variants of the polypeptide, as molecular weight markers for proteins or electrophoresis purpose and the nucleic acid is useful for recombinantly expressing those markers. The polypeptide is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. The nucleic acid is useful as therapeutic agent. PRO is useful in the preparation of RRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful cangents, to construct hybridisation probes for mapping the gene which encodes the PRO and for the generic analysis of individuals with genetic marker, and for generating probes for polymerase chair reaction (PCR), Northern analysis, Southern analysis and Western analysis. PRO antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO in specific cells,

819 240

820 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 760 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAAACCATTTGTT 201 CysyalThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal

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| 8 × 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                       | from recombi<br>antibody is<br>conditions we<br>antibody e- g<br>tissue typin<br>or hypo- or<br>inhibiting tresponse, for<br>treating hea<br>disorders su<br>represents or<br>polypeptide | from recombinant cell culture or natural sources. The polypeptide or its antibody is useful for the preparation of medicament for treating conditions which is responsive to the PRO polypeptide or anti-PRO antibody e.g. tumour. The polypeptide and the nucleic acid is useful for tissue typing. The polypeptide is useful for treating obesity, diabetes to hypo- or hyper-insulinaemia and cardiac insufficiency disorders, for inhibiting tumour growth, enhances vascular permeability and immune response, for inducing reseneration of auditory hair cells and for treating hearing loss in mammals and for treating bone and/or cartilage disorders such as sports injuries and arthritis. The present sequence represents cDNA encoding a human secreted and transmembrane PRO sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other; |
|---------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Alignm<br>Pred.<br>Score:<br>Percen<br>Best L<br>Query<br>DB: | nent Sc<br>No.:<br>it Simi<br>local S<br>Match:                                                                                                                                           | res<br>ari<br>mil                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| US-1                                                          | 0-079-111                                                                                                                                                                                 | 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| λος<br>Op                                                     | 1 160                                                                                                                                                                                     | MetalaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| \$ g                                                          | 21 220                                                                                                                                                                                    | ValGinGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| δλ                                                            | 41                                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| QΩ                                                            | 280                                                                                                                                                                                       | ATCACCCTTGTGAGAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 339                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| 8 8                                                           | 61                                                                                                                                                                                        | CysArgLeuleuGlyLeuSerLeualaGlyLysAspGlnValGluThrAlaLeuLysAla 80                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| Q<br>C                                                        | 340                                                                                                                                                                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| oy<br>d                                                       | 81<br><b>4</b> 00                                                                                                                                                                         | SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArglle 100<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 8 8                                                           | 101                                                                                                                                                                                       | SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal 12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| 3 8                                                           | 121                                                                                                                                                                                       | -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| og qu                                                         | 520                                                                                                                                                                                       | ACCGACAGITIGCAGCCTAITGITACAACTCAICGATACTIGGACTAACTCGTGCATT 57                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| δλ                                                            | 141                                                                                                                                                                                       | ProGluileileThrThrLysAspFroilePheAsnThrGlnThrAlaThrGlnThrThr 160                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| q <sub>C</sub>                                                | 580                                                                                                                                                                                       | CCAGAAATTATCACCACCAAAGATCCCATATTCAACACCAAAACTGCAACACAAACAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| ζ                                                             | 161                                                                                                                                                                                       | GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| q                                                             | 640                                                                                                                                                                                       | CGGTGGCATCCCCTTACTCTACAATA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| δ                                                             | 181                                                                                                                                                                                       | ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| qq                                                            | 700                                                                                                                                                                                       | CCTACTACTACTCCTCCTCCTCCTCCTCTTCTATTCCACGGGGGAAAAAATGATT 759                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |

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GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
  The invention relates to an antibody that binds to a secreted and transmembrane polypeptide, PRO1136. The antibody is useful for preparing an endedicament useful in the treatment of a condition responsive to anti-PRO antibody. The antibody is also useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents a cDNA encoding a PRO polypeptide of the invention
  New monoclonal antibody that binds to a secreted and transmembrane polypeptide, useful for detecting and purifying the polypeptide and also for treating conditions responsive to the antibody.
   160 Arceccacerderreacercererrerrerrerrearerresaceaceacere
   SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
   CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
   520 AGCCGACAGTITGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
  141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
  MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu
  41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
   101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
  460 AGCCCAAACCCCAAGTGTGGGAAAATGGGGTGGGGTGTCCTGATTTGGAAGGTTCCAGTG
   SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
  PJ;
   Godowski
  721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
  2372
322
0
0
0
  Goddard A,
Wood WI;
  Length:
Matches:
Conservative:
Mismatches:
Indels:
   Gaps:
  Ŗ,Ř
  (1-2372)
   Gerritsen |
Watanabe
  Example 4; Fig 5; 235pp; English
  US-10-079-111-1 (1-322) x ACA67273
   1.49e-304
322.00
100.008
100.008
05-JUN-2001; 2001US-00874503.
29-JUN-2001; 2001US-00869599.
18-JUL-2001; 2001US-00908827.
06-DEC-2001; 2001US-00006867.
   Ē,
  (GETH ) GENENTECH INC
   Filvaroff
  Gurney
   WPI; 2003-341840/32.
P-PSDB; ABU81148.
   BP;
  Percent Similarity:
Best Local Similarity:
  Sequence 2372
   ďĊ,
  Alignment Scores:
   Eaton DL,
Grimaldi J
  19
  21
   81
  121
  161
  Query Match:
   Pred. No.:
   Score:
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   염
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  1059
   1119
   300
   939
   280
   999
   320
  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
  1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAAGCT
                                       AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATGATGGAAACC
   AAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
         LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
   AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
   polypeptide PRO263
   Human; gene; ss; affinity purification
  BP.
   99WO-US005028
99US-00311832
99US-00310133
99US-00380138
99US-003801138
99US-00380142
99US-00380142
99US-00403297
   2000US-00644848.
2000WO-US023328.
2000US-00664610.
2000US-00665350.
2000US-0018-0019238.
   2000US-00747259
2000WO-US034956.
2001WO-US006520.
2001US-00816744.
2001US-00854208.
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   2000WO-US005601.
  2000WO-US005841.
2000WO-US007532.
  human secreted
  99WO-US031274
   2000WO-US004341.
   2000WO-US014042
   2000WO-US015264
   2000WO-US030873
   2000WO-US032678
  2001US-00854280
2001US-00870574
  2001WO-US017800
   2002US-00063544
  (first entry)
  GAAGTT 1125
   GluVal 322
   US2003027212-A1
   01-MAR-2000; 22-MAR-2000; 22-MAY-2000; 22-MAY-2000; 22-AUG-2000; 22-AUG-2000; 24-AUG-2000; 24-AU
  cDNA encoding
  14-MAX-1999;
14-MAX-1999;
25-AUG-1999;
25-AUG-1999;
25-AUG-1999;
15-SEP-1999;
16-OCT-1999;
12-NOV-1999;
12-NOV-1999;
13-DEC-1999;
14-MAX-1999;
13-DEC-1999;
14-MAX-1999;
15-MAX-1999;
16-MAX-1999;
16-MA
   10-MAY-2001;
30-MAY-2001;
   02-MAY-2002;
  01-JUN-2001;
   Homo sapiens
  23-JUN-2003
   06-FEB-2003
  1000
  940
   880
   261
  281
  301
   1120
   321
   ACA67273
   RESULT 29
   30-
  ACA67273
```

339

279

9

219

40

20

399 100

80

459 120 519

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The invention describes an isolated polypeptide having at least 80, 85, 95 or 99% identity with: (a) a sequence having 46-335 amino acids, or its extracellular domain; (b) a sequence having 46-335 amino acids, lacking its associated signal peptide; or (c) an amino acid sequence encoded by the full-length coding sequence of the cDNA (ATCC accession number 2095s6). The PRO (secreted and transmembrane) polypeptide is useful for preparing a medicament for treating a condition associated with PRO polypeptide. This sequence encodes a novel human secreted and transmembrane PRO polypeptide
  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArgile 100
  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
   GTCCAAGGCTCTTTGCCTGCACAAGAGCTTTCCATCCAGGGGTGTCATGCAGAATTATGGGG
   ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
   TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
   ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArglleMetGly
   IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
  medicament for treating
   489 G; 638 T; 0 U; 0 Other;
   2372
322
0
0
0
  Goddard A,
Wood WI;
  Length:
Matches:
Conservative:
Mismatches:
  PRO polypeptide, useful for preparing a me condition associated with PRO polypeptide.
  Indels
  Gaps:
  Gerritsen ME,
Watanabe CK,
   US-10-079-111-1 (1-322) x ACH66246 (1-2372)
   Disclosure, Fig 5, 222pp, English.
   721 A; 524 C;
  22-AUG-2000; 2000US-00644848.

24-AUG-2000; 2000US-00664610.

18-SEP-2000; 2000US-00666410.

18-SEP-2000; 2000US-00665350.

08-NOV-2000; 2000US-00709238.

10-NOV-2000; 2000US-00709238.

10-DEC-2000; 2000WO-US030873.

20-DEC-2000; 2000WO-US034956.

28-FEB-2001; 2001WO-US034956.

22-MAR-2001; 2001WS-008154208.

10-MAY-2001; 2001US-00854208.

10-MAY-2001; 2001US-00854209.

10-UN-2001; 2001US-00854209.

10-UN-2001; 2001US-00874503.

29-JUN-2001; 2001US-00874503.

29-JUN-2001; 2001US-00874503.

29-JUN-2001; 2001US-00874503.
  1.49e-304
322.00
100.00%
100.00%
  E,
AL,
  (GETH ) GENENTECH INC
  Filvaroff
   Gurney
   WPI; 2003-456358/43.
   Sequence 2372 BP;
  Percent Similarity:
Best Local Similarity:
  P-PSDB; ABO53263
  Eaton DL, Fi
Grimaldi JC,
   Alignment Scores:
  160
  21
  220
   41
   280
   340
   61
  81
  Query Match:
DB:
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  g
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  1059
   1119
  320
   759
  220
  240
  280
  879
  260
  939
  999
  300
ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuile
  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
   GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
  GAAATTAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAAGGTGTCCCCACGGCTCTG
  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr
  .000 AAAGTAGTAAAAGGAGGAGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAAACT
  AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
  GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAAACTACCGTGCCGATGCCTGGAAGGT
   rereteacadatrirrargaaacrageaccarereragaaacraaaccarrirer
   ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
   Novel human secreted and transmembrane protein PRO263 cDNA.
  SS
   transmembrane protein; PRO; gene;
  BP.
   ACH66246 standard; cDNA; 2372
  99WO-US005028
99WS-00311832
99WS-00380137
99WS-00380139
99WS-00380139
99WS-003973422
99WS-00403297
99WS-00403297
  2000WO-US007532.
2000WO-US014042.
2000WO-US015264.
   2000WO-US004341.
2000WO-US005601.
2000WO-US005841.
  2002US-00063549
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   1120 GAAGTT 1125
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  GluVal 322
  US2003027986-A1
   21-MAR-2000;
22-MAY-2000;
02-JUN-2000;
  Homo sapiens
  02-MAY-2002;
  08-MAX-1999;
14-MAY-1999;
14-MAY-1999;
25-AUG-1999;
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  01-MAR-2000;
02-MAR-2000;
  18-FEB-2000;
  12-NOV-1999;
30-DEC-1999;
   14-OCT-2003
   15-SEP-1999
  06-FEB-2003
  261
   281
              640
   700
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   760
  221
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  321
                                     181
   301
   1060
   ACH66246;
   Human;
   RESULT 30
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Godowski

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1059
   220
  240
  260
   939
   280
   999
   300
  Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy; cancer; chromosome mapping; gene mapping; diagnostic; biosensor; bioreactor; gene; ss.
  819
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  519
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  CCAGAAATTATCACCACAAAGATCCCATATTCAACACTCAAACTGCAAACAACA 639
  GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
  669
   ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle 200
   759
400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTTAGGATT 459
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  1000 AAAGTAGTAAAGGAGGAGAAAGGAGCCAATGATAGCAACCCTAATGAGGAATCAAAAGT
  GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLyS
   880 craciccriticriticriticriticardiccicciccricicriticariticara
  940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
  AGCCCAAACCCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
   CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
  TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAAACCATTTGTT
   ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
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   02-MAY-2002; 2002US-00063530
   98KR-00062142
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   30-JUL-2003
  05-DEC-2002
  281
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  460
   520
  580
  161
   640
   181
   700
  760
   261
  301
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2000US-00747259.
2000WO-US034956.
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2001US-00B16744.
2001US-00B54208.
2001US-00B54280.
   99US-00397342.
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99US-00423844.
   2001US-00874503.
2001US-00869599.
2001US-00908827.
  2000US-00644848.
2000WO-US023328.
   2000US-00665350.
2000US-00709238.
  2001WO-US017800.
                                       99WO-US010733.
  99WO-US031274
  2000WO-US004341
  2000WO-US005601
   2000WO-US005841
   2000WO-US007532
  2000WO-US014042
  2000WO-US015264
   2000US-00664610
  2000WO-US030873
  2000WO-US032678
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   20-DEC-2000;
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28-FEB-2001;
22-MAR-2001;
  25-AUG-1999;
25-AUG-1999;
25-AUG-1999;
15-SEP-1999;
  01-JUN-2001;
   29-JUN-2001;
18-JUL-2001;
   ,666
  30-DEC-1999;
   12-NOV-1999
```

## (GETH ) GENENTECH INC.

Goddard A, Godowski PJ; Wood WI; Gerritsen ME, Watanabe CK, lvaroff E, Gurney AL, Filvaroff Grimaldi JC, DI, Eaton

2003-328636/31,

P-PSDB; ABU98265.

preparing a medicament for treating a condition, e.g. cancer, responsive to the antibody, and in diagnostic and purification assays for the PRO New antibody that specifically binds to a PRO polypeptide, useful in polypeptide

Disclosure, Fig 5; 236pp; English.

The invention describes an antibody that binds to a polypeptide having a sequence of 277 amino acids fully defined in the specification. The antibody, PRO polypeptide, or the agonist or antagonist of the collipseptide, is useful in preparing a medicament for treating a condition responsive to the PRO polypeptide, agonist or antagonist, or the antibody, such as cancer. The antibody may also be used in diagnostic assays for PRO polypeptide in specific cells, tissue or serum, and in affinity purification of the polypeptide. The nucleic acid molecule is useful in molecular biology, as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO colypeptide by recombinant techniques, and in gene therapy. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences or as antisense probes. The secreted proteins are useful in industrial applications, including as pharmaceuticals, diagnostics, blosensors and bloreactors. The PRO polypeptides may also be employed as molecular weight markers for protein electrophoresis PRO polypeptide

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

```
New PRO polypeptide and the nucleic acid encoding the PRO polypeptide,
  ss.
  PJ;
  Human; secreted and transmembrane protein; PRO; ATCC 209902; gene therapy; chromosome identification; tissue typing; gene;
  Godowski
  Novel human secreted and transmembrane protein PR0263 cDNA
  Goddard A,
Wood WI;
  ĊΚ,
  Gerritsen
Watanabe
  ACA89291 standard; cDNA; 2372 BP.
  14 MAY - 1999; 9905-00310137.
25-AUG-1999; 9905-00380139.
25-AUG-1999; 9905-00380139.
25-AUG-1999; 9905-00380138.
25-AUG-1999; 9905-00380138.
25-AUG-1999; 9905-00380142.
18-CCT-1999; 9905-00403297.
18-CCT-1999; 9905-00403297.
21-NAX-2000; 2000WO-US001541.
21-MAX-2000; 2000WO-US005601.
21-MAX-2000; 2000WO-US005601.
22-MG-2000; 2000WO-US01528.
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23-AUG-2000; 2000WO-US01528.
24-AUG-2000; 2000WO-US0380873.
01-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2000WO-US034956.
20-DEC-2000; 2000WO-US034956.
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99WO-US005028.
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99US-00380138.
99US-00380139.
   18-JUL-2001; 2001US-00908827
06-DEC-2001; 2001US-00006867
  (first entry)
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AL,
  (GETH ) GENENTECH INC
   Filvaroff
C, Gurney
   GAAGTT 1125
  WPI; 2003-332052/31.
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                GluVal 322
   US2003036634-A1.
  Homo sapiens.
  02-MAY-2002;
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Grimaldi JC,
  08-JUL-2003
  20-FEB-2003
   ACA89291;
   1120
                321
   30-I
   ACA8929
  1059
   1119
  240
  320
   279
  399
   100
   459
   SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
   519
  140
   579
  160
  639
   180
  669
  200
   759
  220
   819
   879
   280
  999
   300
  939
  20
  40
  9
   80
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  MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu
   ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG
   ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
  GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
  41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAla
   CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuIysAla
   TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArgile
   SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
  ACCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
   ProGlullelleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr
   GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
  GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
  CCTACTACTACTCCTCCTCCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT
   GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
   820 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaAlaGlyLeuGlyPheCysTyrValLys
   880 cradificationicitationicitationicalecticationical
   940 AGGTATGTGAAGGCCTTCCCTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACC
  301 AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla
  1060 GATAAAAACCCAGAAGAGTCCAAGGAAAACTACCGTGCGATGCCTGGAAGCT
  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
  261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
            2372
322
0
0
0
                                       Conservative:
Mismatches:
Indels:
Gaps:
             Length:
Matches:
   (1-2372)
   US-10-079-111-1 (1-322) x ACD02300
    1.49e-304
322.00
100.008
100.008
                                     Percent Similarity:
Best Local Similarity:
Alignment Scores:
   640
   -
  160
   21
  220
  280
   61
   340
  81
   100
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  460
   121
  520
  141
  161
   181
  200
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  281
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   221
  Query Match:
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320

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GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTG
  AGGTATGTGAAGGCCTTCCCTTTTACAAAGAATCAGGAGAAGGAAATGATGGAAAACC
  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
  1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAAACTACCGTGCGATGCCTGGAAGCT
   AAAGTAGTAAAGGAGGAGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
   AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
  transmembrane protein; PRO; cytostatic;
   Novel human secreted and transmembrane protein PRO263 cDNA.
   BP
   immunotherapy; cancer; gene; ss
   ACA68928 standard; cDNA; 2372
   9905-00311832-
9905-00311832-
9905-00380137-
9905-00380139-
9905-00380142-
9905-00403297-
  2000WO-US004341.
2000WO-US005601.
2000WO-US005841.
2000WO-US007532.
  2000WO-US014042.
2000WO-US015264.
2000US-00644848.
2000WO-US023328.
   2000US-00664610.
   2000US-00747259.
2000WO-US034956.
  2001WO-US006520.
2001US-00816744.
  2000US-00665350
   2002US-00063551
   99WO-US031274
   2000WO-US030873
  2001US-00854208
  (first entry)
   1120 GAAGTT 1125
  secreted and
  GluVal 322
  US2002183494-A1
  18-FEB-2000;
01-MAR-2000;
02-MAR-2000;
21-MAR-2000;
   25-AUG-1999;
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25-AUG-1999;
25-AUG-1999;
15-SEP-1999;
  22-MAR-2001;
10-MAY-2001;
  18-OCT-1999;
12-NOV-1999;
30-DEC-1999;
  22-MAY-2000;
02-JUN-2000;
   22-AUG-2000;
24-AUG-2000;
  08-NOV-2000;
   10-NOV-2000;
   02-MAY-2002;
   26-JUN-2003
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   The invention describes an isolated polypeptide comprising 80 % amino acid sequence identity with: (a) a sequence comprising 556 amino acids, given in the specification, or its extracellular domain, with or without its associated signal peptide; or (b) a sequence of a polypeptide encoded by a full-length coding sequence of the cDNA deposited under American Type Culture Collection (ATCC) accession number 209902. The new PRO polypeptide or the nucleic acid encoding the PRO polypeptide is useful in gene therapy, for chromosome identification or for tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide
  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
   279
  339
   399
  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile 100
  459
   120
   519
  140
  579
   ProGlullelleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr 160
  639
   GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
  669
   200
  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
  819
   40
  9
   80
   20
  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuile
   CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT
  MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu
   ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArglleMetGly
  GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
  11eThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
   CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
  AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
  TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
  TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
   AGCTTTGAAACTTGCAGCTATGGCTTGGAGATGGATTCGTGGTCATCTTAGGATT
   SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
   SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
for chromosome identification or for tissue
  721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
   2372
322
0
0
0
   Length:
Matches:
Conservative:
Mismatches:
Indels:
   Gaps:
   x ACA89291 (1-2372)
  Disclosure, Fig 5; 235pp; English.
   1,49e-304
322.00
100.00$
100.00$
 in gene therapy,
   US-10-079-111-1 (1-322)
  BP;
  Percent Similarity:
Best Local Similarity:
  Sequence 2372
  Alignment Scores:
Pred. No.:
Score:
   280
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   094
  220
  41
   61
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   400
  460
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   141
   640
  181
  201
   221
   21
  81
   121
  580
   161
   101
  Query Match:
DB:
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1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT 1119
   819
  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGerLysLysThr 300
   879
  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
   940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 999
   LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
                      GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
   GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
  aProAlaSerThrSerIleProArgArgLysLysLe
   GABABTABABCAGCATTCABGBATGABGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTG
   <u>AAAGTAGTAAAGGAGGAGGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT</u>
   AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
  ceraciaeraerecreerecreericeaerrecreeringiani
   TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
  CTAGTGCTTGCTCTCTTTTGGTGCTGCTGGTCTTGGATTTTTGCTATGTCAAA
   CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
  enterocolitis; gastrointestinal ulceration; skin disease; keratinocyte differentiation; epithelial cancer; Alzheimer's disease squamous cell carcinoma; Parkinson's disease; inflammatory disease; amyotrophic lateral sclerosis; rheumatoid arthritis; asthma; multiple sclerosis; organ failure; atherosclerosis; cardiac injury; inflattility; birth defect; premacure aging; AlDS; cancer; diabetic complication; wound repair; tissue re-growth; gene; ss.
   Human; secreted and transmembrane protein; gene therapy; psoriasis;
  Novel human secreted and transmembrane protein PRO263 cDNA
  BP.
   970S-0059113P.
970S-0059115P.
970S-0059119P.
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970S-0059128P.
970S-0059263P.
  standard; cDNA; 2372
   2001US-00903640
  (first entry)
   GAAGTT 1125
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  US2003017463-A1.
  17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
18-SEP-1997;
18-SEP-1997;
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   11-JUL-2001;
  05-JUN-2003
  23-JAN-2003
   17-SEP-1997
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   640
  200
  221
   241
  880
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  281
   1000
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  ACA54972
  RESULT 34
   ACA54972
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  The invention describes an antibody that binds to a novel human secreted and transmembrane PRO polypeptide. The antibody is useful in preparing a medicament for treating a condition e.g. cancer. The antibody may also be used in diagnostic assays for PRO polypeptide in specific cells, tissue or serum, and in affinity purification of the polypeptide. This sequence encodes a novel human secreted and transmembrane PRO polypeptide
   219
  279
  339
   399
   120
   519
  140
   160
   100
  459
  639
  New antibody that specifically binds to a PRO polypeptide, useful in preparing a medicament for treating a condition, e.g. cancer, responsive to the antibody, and in diagnostic and purification assays for the PRO
  20
  40
   9
  80
   Arggecaggrachreacchegrangerrereachrecarchegachegaechere
   GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
   SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle
   ProGluIleIleThrThrLy8AspProIlePheAsnThrGlnThrAlaThrGlnThrThr
   CCAGABATTATCACCACCABABGATCCCATATTCAACACTCCAAACTGCAACAACAACA
  MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu
   IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
  TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAAAGCT
   SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal
   AGCCCAAACCCCAAGTGTGGGAAAATGGGGTGTGTCCTGATTTGGAAGGTTCCAGTG
  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
   ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
  AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
  100 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTTAGGATT
  Godowski PJ;
  BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
  2372
322
0
0
0
  Goddard A,
Wood WI;
  Length:
Matches:
Conservative:
Mismatches:
  Indels:
   Gaps:
  Gerritsen ME,
Watanabe CK,
  (1-2372)
  Disclosure; Fig 5; 235pp; English.
10-MAY-2001; 2001US-00854280.
30-MAY-2001; 2001US-00870574.
01-JUN-2001; 2001US-008714503.
05-JUN-2001; 2001US-00874503.
29-JUN-2001; 2001US-00968959.
18-JUL-2001; 2001US-00908827.
06-DEC-2001; 2001US-00906867.
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322.00
100.00%
100.00%
100.00%
  Filvaroff E,
   (GETH ) GENENTECH INC
  WPI; 2003-340981/32.
P-PSDB; ABU82477.
  Best Local Similarity:
   Percent Similarity:
  Sequence 2372
   JC,
   Alignment Scores:
  polypeptide
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Grimaldi
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   160
  220
   41
   280
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   141
  580
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  121
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98WO-US019437
98US-0104080P
98US-0109304P.
98WO-US025108
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99US-0145698P.
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970S-006373P.
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98WO-US019177.
  99WO-US020944.
   99WO-US028214.
  98WO-US019330.
98US-0100858P.
   99WO-US021547.
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   05-JAN-2000; 2000WO-US000219
11-FEB-2000; 2000WO-US003565
22-FEB-2000; 2000WO-US004414
   99WO-US020594
   99WO-US028313
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  01-DEC-1998
  07-JUL-1999
   28-JUL-1999;
08-SEP-1999;
   DEC-1999
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New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ fallure, atheroscherosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease.
  , Botstein D, Desnoyers L, Eaton DL, Ferrara N; , Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; , Wood WI;
  Claim 2; Fig 73; 473pp; English.
                            2000WO-US008439.
2000WO-US014042.
2000WO-US015264.
2000WO-US020710.
2000WO-US023328.
          2000WO-US005841.
2000WO-US007377.
   2000US-00665350
   (GETH ) GENENTECH INC.
   WPI; 2003-341586/32.
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24-FEB-2000; 2
02-MAR-2000; 2
30-MAR-2000; 2
30-MAR-2000; 2
22-MAY-2000; 2
24-UUJ-2000; 2
24-AUG-2000; 2
   18-SEP-2000;
   Godowski PJ,
  Williams PM,
   Ashkenazi A,
Filvaroff E,
   Mather JP,
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or

The invention describes sixty one nucleic acids encoding PRO polypeptides (secreted and transmembrane). The PRO polypeptides and nucleic acids are useful in diagnosing or treating enterocolitis, gastrointestinal culceration, skin diseases associated with abnormal keratinocyte ulceration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoriasis or epithalial cancers such as squamous cell carcinoma, Alzheimer's disease, e.g. rheumatoid arthritis, cathma or multiple sclerosis, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, ALDS, cancer, diabetic complications, or mutations in general. The polypeptides are also useful for wound repair and associated therapies concerned with region useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This sequence encodes a convertible control of the protein accombinant cell culture or natural sources. This sequence encodes a 280 ATCACCCTTGTGAGAGAGAAAAAGGCGAACCAGCAGAATTTCACAGAAGCTAAGGAGGGC 339 160 ATGGCCAGGTGCTTCAGCCTGGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 220 GICCAAGGCICTIIGCGIGCAGAAGAGCIIICCAICCAGGIGICAIGCAGAAIIAIGGGG 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other; 2372 322 0 0 0 Length:
Matches:
Conservative:
Mismatches: Indels: Gaps: US-10-079-111-1 (1-322) x ACA54972 (1-2372) 1.49e-304 322.00 100.00% 100.00% Best Local Similarity: Query Match: Percent Similarity: Alignment Scores: 21 Pred. No.: Score: qq 엄 à à ò

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340 TGTAGGCTGCGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla

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New anti-PRO antibody, useful in diagnostic assays for PRO polypeptide for affinity purification of PRO from the recombinant cell culture or
   The invention relates to an antibody which binds to a PRO polypeptide. The antibody is useful in diagnostic assays for the PRO polypeptide or for affinity purification of PRO from a recombinant cell culture or natural source. Sequences ACA98448-ACA98531 represent CNA molecules
  PJ;
  Godowski
  U; 0 Other;
   2372
322
0
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   Ą,
  Goddard A
  Length:
Matches:
Conservative:
Mismatches:
Indels:
   encoding human PRO polypeptides of the invention
   721 A; 524 C; 489 G; 638 T; 0
  Gaps:
  Ä,Ÿ
   x ACA98450 (1-2372)
  Gerritsen
Watanabe
  Disclosure; Fig 5; 236pp; English.
  01-MAR-2000; 2000MO-US005601.
02-MAR-2000; 2000MO-US005841.
02-MAR-2000; 2000MO-US005841.
02-MAY-2000; 2000MO-US014042.
02-JUN-2000; 2000MO-US01564.
04-MUG-2000; 2000US-0064848.
18-SEP-2000; 2000US-00664510.
18-SEP-2000; 2000US-0066510.
19-NOV-2000; 2000US-00709238.
10-NOV-2000; 2000US-00709238.
10-NOV-2000; 2000WO-US03678.
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22-DEC-2000; 2000WO-US034956.
23-PER-2001; 2001WS-00816744.
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10-MAY-2001; 2001WS-0081674.
10-MAY-2001; 2001WS-0081674.
10-MAY-2001; 2001WS-0081674.
01-UN-2001; 2001WS-0081659.
18-JUL-2001; 2001WS-00869599.
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990S-00380138.
990S-00380142.
990S-00397342.
990S-00403297.
  99US-00423844.
99WO-US031274.
2000WO-US004341.
 99WO-US0050142.
99WO-US005028.
99US-00311832.
99WO-US010733.
   1.49e-304
322.00
100.00%
100.00%
  Ē,
   Filvaroff I
  (GETH ) GENENTECH INC
  WPI; 2003-417284/39.
   BP;
  US-10-079-111-1 (1-322)
   Percent Similarity:
Best Local Similarity:
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25-AUG-1999;
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115-SEP-1999;
116-SEP-1999;
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118-SEP-1999;
118-SEP-1999;
118-SEP-1999;
118-SEP-1999;
118-SEP-1999;
   JC,
  Alignment Scores:
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  Grimaldi
   Eaton
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  1059
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   200
   759
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  260
   280
  999
  300
  320
           SerPheGluThrCysSerTyrGlyTrpValGJyAspGlyPheValValIleSerArgIle
                          AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGTTGGATTCGTGGTCATCTTTAGGATT
  AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTGTCCTGATTGGAAGGTTCCAGTG
  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCyslle
   ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
  CCAGAAATTATCACCACCAACAAGATCCCATATTCAACACTCAAACTGCAACACAACAACAACA
  GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThr1leProAla
  GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
   ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
   GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
   LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
   CTAGTGCTTGCTCCTCTTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA
  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
   1000 AAGTAAGGAAGAGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT
   AsplysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla
  1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAAGCT
  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal
  TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
   940 AGGIATGIGAAGGCCITCCCTITIACAACAAGAATCAGCAGAAGGAAATGATCGAAACC
  Human; PRO; gene; ss; affinity purification.
   ВP
   2372
  02-MAY-2002; 2002US-00063537
   Human PRO polynucleotide #3
   entry)
   standard; cDNA;
  1120 GAAGTT 1125
   GluVal 322
  (first
   US2003027993-A1
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   25-JUL-2003
  06-FEB-2003
   640
                                   400
   460
   121
  520
   141
  580
   700
  760
  221
   820
   321
            81
   101
   161
   181
  201
   241
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   ACA98450
   ACA98450;
  RESULT 35
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The present invention relates to the isolation of novel human PRO polypeptides, and the polypucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of a condition responsive to anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ACA63373-ACA63456 represent cDNA sequences encoding the human PRO polypeptides of the invention
   GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
   CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
  MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu
  41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
   ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
   TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
   AGCTITIGAAACTIGCAGCTAGGCTIGGAGAIGGATICGIGGICAICTCTAGGATT
  Novel monoclonal antibody that binds to secreted and transmembrane polypeptide, useful for detecting and purifying the polypeptide and for treating conditions responsive to the antibody.
  Godowski PJ;
                          Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; gene;
   U; 0 Other;
   2372
322
0
0
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  Goddard A,
Wood WI;
  0
   Conservative:
Mismatches:
   .
H
   Length:
Matches:
   BP; 721 A; 524 C; 489 G; 638
  Indels:
Gaps:
  Gerritsen ME,
Watanabe CK,
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encoding human PRO polypeptide
  Disclosure; Fig 5; 408pp; English
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  1.49e-304
322.00
100.00%
100.00%
100.00%
  01-MAY-2002; 2002US-00063502
   06-DEC-2001; 2001US-00006867.
  E,
AL,
   (GETH ) GENENTECH INC
  Filvaroff
  Gurney
  2003-331484/31.
  Best Local Similarity:
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  US2003023042-A1
  Eaton DL, Fil
Grimaldi JC,
   Percent Similarity:
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  sapiens
  Alignment Scores:
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   160
  220
  280
   340
   21
   61
  81
   400
  101
  Query Match:
DB:
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   180
                                       279
  TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAGTTGAAACAGCCTTGAAAGCT 399
  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
   459
  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
   519
   140
  579
   ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
  639
   GAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCCTTACTCTACATACCTGCC 699
  200
   220
   GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
  879
  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
  939
   280
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                                   220 Grccaaggcrcrrrgcgrgcagaagagcrrrccarccaggrgrcargcagaarrarggg
  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
   GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
   AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
   GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGGAAGCT
   460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
  520 Acceacactriceaecerarierracaacrearcrearacrissacraacresiscarr
  ccadaaartrarcaccaccaagarcccararrcaacacrcaaacrgcaacacaacaaca
   ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle
   CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
  chadrectricarctricardargerecreateraterargerargerena
  AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
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   ACA63375
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98WO-US019177.
  98WO-US019437.
98US-0104080P.
98US-0109304P.
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98US-0113296P.
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  99WO-US021547
  99WO-US028214
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22-DEC-1998;
   13-SEP-1999;
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15-SEP-1999;
  05-OCT-1999;
29-NOV-1999;
   17-SEP-1997
   08-SEP-1999
    1059
  1119
  Human; ss; gene; gene therapy; apoptosis; bleeding; tumour; ALS; gynaecological disease; hysterectomy; angiogenesis; skin disease; cancer; coronary ischaemic condition; gastrointestinal mucosa disorder; asthma; mucosal lesion repair; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; neurogathy; blood cosquiation cascade disorder; thrombosis; haemorrhage; neurodegenerative disease; endometrial bleeding; wound healing; tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing.
                   519
  160
   639
   180
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  200
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   220
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  240
   879
   260
   939
  280
  666
   300
  AsplysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
                    AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
   GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThr1leProAla
   TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTGTT
   GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGTTTTGGAGGTGTCCCCACGGCTCTG
   LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
   CTAGTGCCTTGCTCTCTTTTGGTGCTGCAGCTGGTCTTTGGATTTTGCTATGTAAA
  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
   AAAGTAGTAAAGGAGGAGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
   AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
  GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
   GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
   GATAAAAACCCAGAAGAGTCCAAGAGCAAAACTACCGTGCGATGCCTGGAAGCT
   CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
Human secreted / transmembrane polypeptide PRO263 cDNA.
   ACD19807 standard; cDNA; 2372 BP
  16-JUL-2001; 2001US-00906838.
  (first entry)
  GAAGTT 1125
   GluVal 322
   US2003027143-A1
  Homo sapiens
  22-AUG-2003
  06-FEB-2003
                 460
  640
   940
  1000
   1060
  1120
   580
  160
   ACD19807;
   121
  520
  141
  161
  181
   700
  201
  221
   820
   241
  261
   281
  301
   321
  RESULT 37
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30-NOV-1999; 99WO-USC28313.

01-DEC-1999; 99WO-USC28301.

02-DEC-1999; 99WO-USC28564.

02-DEC-1999; 99WO-USC30095.

16-DEC-1999; 99WO-USC30091.

20-DEC-1999; 99WO-USC30091.

20-DEC-1999; 99WO-USC30091.

20-DEC-1999; 99WO-USC30091.

21-FEB-2000; 2000WO-USC00565.

22-FEB-2000; 2000WO-USC06561.

24-FEB-2000; 2000WO-USC06641.

20-MAR-2000; 2000WO-USC06841.

20-MAR-2000; 2000WO-USC06841.

20-MAR-2000; 2000WO-USC06841.

20-MAR-2000; 2000WO-USC06841.
  2000WO-US014042.
2000WO-US015264.
2000WO-US020710.
2000WO-US023328.
   (GETH ) GENENTECH INC.
  Wood WI;
  WPI; 2003-417249/39.
P-PSDB; ABO14839.
   Ashkenazi A, Botste
Filvaroff E, Fong (Godowski PJ, Grima
Mather JP, Pan J,
  Williams PM,
   28-JUL-2000;
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Ferrara N; ME, Goddard A; Kljavin IJ; Tumas D; , Botstein D, Desnoyers L, Baton DL, I Fong S, Gao W, Gerber H, Gerritsen P, Grimaldi JC, Gurney AL, Hillan KJ, I Pan J, Paoni NF, Roy MA, Stewart TA,

Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases

Claim 2; Fig 73; 467pp; English.

polypeptide. The PRO polypeptides are useful for modulating biological activity of a cell, in diagnosing or treating abnormal bleeding involved in gynaecological diseases e.g. to avoid or lessen the need for thysterectomy, for treating anglogenesis, tumour, coronary ischaemic or hysterectomy, for treating anglogenesis, tumour, coronary ischaemic condition, disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's cascade disorders, neurodegenerative disease, thrombosis, haemorrhage, endometrial bleeding, wound healing, tissue repair, asthma, rheumatoid arthritis, multiple sclerosis. Nucleic acid encoding PRO polypeptides are useful in molecular biology including uses as hybridisation probes and includes are useful in molecular animals or knockout animals. The PRO antibodies are useful for tissue typing. PRO antibodies are useful in diagnostic assays for sample fluids. Anti-PRO antibodies are useful in diagnostic assays for sample fluids. Anti-PRO antibodies are useful in diagnostic assays for sources. The present sequence represents conding a human secreted condinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents conding a human secreted and transmembrane PRO polypeptide invention relates to an isolated secreted and transmembrane PRO

U; 0 Other; Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0

| Length: 237                     | Matches: 322 | Conservative: 0 | Mismatches: 0 | lels: 0      | 0 :30 |
|---------------------------------|--------------|-----------------|---------------|--------------|-------|
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| Alignment Scores:<br>Pred. No.: |              |                 | ty:           | Query Match: | DB: 8 |

US-10-079-111-1 (1-322) x ACD19807 (1-2372)

1059 1119 160 219 279 100 459 120 140 579 639 180 669 200 759 220 819 240 879 260 939 339 340 IGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399 280 999 300 40 20 9 80 160 ATGGCCAGGTGCTTCAGCCTGGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 220 GICCAAGGCICITIGCGIGCAGAAGAGCTITICCAICCAGGIGICAIGCAGAATTAIGGGG 280 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCGGAGCTGAATTTCACAGAGAGCTCA SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle ProGluIleIleThrTysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 700 CCTACTACTACTCCTCCTCCTCCCCACTTCCACTTCCACTTCCACGAGAAAAATTGATT TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTGTT GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 820 GAAAATAAAAGCAGCATTCAAGAATGAAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTACAATACCTGCC CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 460 AGCCCAAACCCCAAGTGTGGAAAATGGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG 520 AGCCGACAGTITGCAGCCTAITGTIACAACTCAICGATACTIGGACTAACTCGGGCAIT ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 880 CIAGTGCTTCTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTAAA 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 1000 AAAGTAGTAAAGGAGGAGAAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGAAAACT AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT GAAGTT 1125 GluVal 322 241 21 160 41 61 81 101 121 141 161 221 281 301 321 1120 181 201 RESULT 38 g gg d g g à g ò g à g à g ò ò δ 셤 à ò g 8 g ò g à g à g ð g à 임

ADB29405 standard; cDNA; 2372 BP. ADB29405 ID ADB2 XX

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Human; gene; ss; PRO; secreted; transmembrane; gastrointestinal mucosa; mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding anglogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
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   9703-0059113P.
9703-0059113P.
9703-0059111P.
9703-0059111P.
9703-0059112P.
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9703-0059121P.
9703-0059124P.
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9703-0062285P.
9703-0062312P.
9703-0062312P.
9703-0062312P.
9703-0063312P.
9703-006332P.
9703-006332P.
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9703-006332P.
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9703-006373P.
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   US2003092002-A1.
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  21-0CT-1997;
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   24-NOV-1997;
25-NOV-1997;
  17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
   15-MAY-2003
  17-NOV-1997
  17-SEP-1997
ADB29405;
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11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US0036414.
24-FEB-2000; 2000WO-US005644.
20-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US003377.
30-MAR-2000; 2000WO-US003377.
   99WO-US028564.
99WO-US028565.
99WO-US030095.
   98US-0088026P.
98US-0099803P.
98WO-US018824.
   98US-0100262P.
98WO-US019177.
98WO-US019330.
  98US-0113296P.
99US-0143048P.
  99WO-US020944
99WO-US021090
  99WO-US028313
99WO-US028301
   2000WO-US000219.
  98US-0100858P
98WO-US019437
   98US-0109304P
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  99US-0146222P
  99WO-US020594
   99WO-US021547
   99WO-US023089
  99WO-US028214
  99WO-US030911
   99WO-US030999
  22-MAY-2000; 2000WO-US014042
02-JUN-2000; 2000WO-US015264
   28-JUL-2000; 2000WO-US020710
24-AUG-2000; 2000WO-US023328
  30-NOV-1999;
01-DEC-1999;
02-DEC-1999;
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20-DEC-1999;
05-JAN-2000;
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10-SEP-1998;
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14-SEP-1998;
16-SEP-1998;
  17-SEP-1998
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26-JUL-1999
08-SEP-1999
   13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
29-NOV-1999;
```

#### (GETH ) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

#### WPI; 2003-765473/72. P-PSDB; ADB29406.

Novel isolated native PRO polypeptide useful for treating Parkinson's disease, enterocolitis, Zollinger-Ellison syndrome gastrointestinal ulceration, Alzheimer's disease, amyotrophic lateral sclerosis, Usher syndrome.

## Claim 2; Fig 73; 469pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO polypeptide, for linking a at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. PRO polypeptides are also useful for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte

diseases, amyotrophic lateral sclerosis (ALS), neuropathies and additionally, disease related to uncontrolled cell growth, e.g. cancer. PRO polypeptides also serves as tumour specific antigens which may be exploited as therapeutic targets for anti-tumour drugs, and are also employed therapeutic targets for anti-tumour drugs, and are also comployed therapeutically in vivo for lessening the effects of viral infection. The PRO polypeptides can be also used in assays to determine if it has a role in neurodegenerative diseases or their reversal, as an antithrombotic agent with reduced risk for haemorrhage as compared with hepatin, in treating other PRO associated disorders, in modulating concentrial bleeding angiogenesis, and may also have an effect on kidney tissue. PRO polypeptides and their portions affect the expression of tissue. PRO polypeptides and their portions affect the expression of concentrial bloody including uses as hybridisation probes for cDNA library to isolate the full-length PRO cDNA or to isolate other cDNAs, in concentrial proparing PRO polypeptides, for generation of antisense RNA and DNA, for preparing PRO polypeptides, for generation of antisense RNA and DNA, concentrial and gene mapping, in the generation of antisense RNA and DNA, concentrial and generation and for chromosome and for the generation of antisense RNA and DNA, concentrial as molecular marker for protein electrophoresis purposes, as therapeutic agents, for screening compounds to identify those that mimic the PRO polypeptide (antagonists) or prevent the effect of the PRO consequent concentrial and concentrial controlled and concentrial and concentrate recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a gene encoding a PRO polynucleotide of the 

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

160 ArGGCCAGGTGCTTCAGCCTGGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219 220 Grcchadgertringcengchagagerintcanccagerercangeagannarges 279 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArgile 100 100 AGCTITIGAAACTIGCAGCIAIGGCIGGGIIGGAGAIGGAITCGIGGICAICTCIAGGAIT 459 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 579 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20 40 9 80 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 322 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: x ADB29405 (1-2372) 1.49e - 304322.00 100.00% 100.00% 100.00% US-10-079-111-1 (1-322) Similarity: Percent Similarity: Best Local Similari 21 61 81 101 460 121 Query Match: DB: ò g à g ò g ò a ठे g ò g à

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1119
                            639
  180
   669
   220
   240
  260
  666
  300
  301 AsplysAsnProGluGluSerLysSerProSerLysThrTyalArgCysLeuGluAla 320
   879
   939
   PRO; transmembrane; immunoconjugate; cytotoxic; gene therapy;
               580 CCAGAAATTATCACCACCAACAAGATCCCCATATTCAACACTACAACTGCAACACAACAA
  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
   880 CTAGTGCTTGCTCTCCTCTTTGGTGCTGCTGGTCTTGGTTTTTGCTATGTAAAA
ProGlullelleThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr
  161 GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
   640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
   ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
  700 CCTACTACTACTCCTCCTCCTCCTCCTCCTCTTCTATTCCACGAGAAAAAATTGATT
   CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
   760 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
  820 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
  940 AGGIATGIGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACC
  281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
   1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGAGCAAAACTACCGIGCGATGCCTGGAAGCT
  261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.
   ADB17062 standard; cDNA; 2372 BP
  99WO-US010733.
   99US-00380138.
  2002US-00063598
  98KR-00062142
99WO-US005028
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  99US-00380142
   99US-00397342
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99US-00423844
  99WO-US031274
  (first entry)
   ss; gene; PRO; transmembra cytostatic; cancer; human.
  1120 GAAGTT 1125
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  03-MAY-2002;
  20-NOV-2003
  30-DEC-1998;
08-MAR-1999;
  14-MAY-1999;
25-AUG-1999;
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180

200

819 240 879 260

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1000 AAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT 1059
   SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 279
  340 reradecrecreseacraacrirescesedaaseaccaastreaaacasecrreaaaser
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  CTAGTGCTTGCTCTCCTCTTTGGTGCTGCTGCTGGTCTTTGGATTTTGCTATGTCAAA
   1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAACAAAACTACCGTGCGATGCCTGGAAGCT
                         IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile
   ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
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   940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
   301 AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
   SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
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   Human; ss; tumour; cancer; tissue typing; gene.
  ВР
  standard; cDNA; 2372
   (first entry)
  1125
   GluVal 322
  1120 GAAGTT
  26-SEP-2003
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   820
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  460
  580
  700
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  61
   81
   101
   121
   141
  161
   181
  201
   094
  221
  241
   261
   ACH03578;
  Human
  g
   g
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  셤
  셤
  셤
  qq
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  MXEXEXEX BXB
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   This invention relates to a novel isolated and secreted PRO polypeptide. PRO is a transmembrane protein involved in the formation, differentiation and maintenance of multicellular organisms, and more particularly the proliferation, differentiation and migration of individual cells. The invention describes screening compounds to identify PRO polypeptide agonists and antagonists, anti-PRO antibodies, and immunocollugates comprishing an antibody conjugated to a cyctotoxic agent. Specifically, the hetrologous protein of the chimeric polypeptide is an epicope tag or an PC region of an immunoglobulin. Through the use of gene therapy, the PRO polypeptide is useful for preparing cytostatic compositions for diagnosing or treating cancer. The polypeptide is also useful as a molecular weight marker for protein electrophoresis purposes. This polypeptide, found in the CDNA library of the invention.
  40
   New secreted and transmembrane PRO polypeptide, useful for preparing a composition for diagnosing or treating cancer and as a molecular weight marker.
   ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
   Godowski PJ;
  U; 0 Other;
   2372
322
0
0
0
   Goddard A,
Wood WI;
  Length:
Matches:
Conservative:
Mismatches:
Indels:
  489 G; 638 T; 0
   Gaps:
   Gerritsen ME,
Watanabe CK,
   US-10-079-111-1 (1-322) x ADB17062 (1-2372)
   Disclosure; Fig 5; 235pp; English
  Sequence 2372 BP; 721 A; 524 C;
   2001WO-US017800
2001US-00874503.
2001US-00869599.
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2001WO-US006520.
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Grimaldi JC,
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02-MAR-2000;
   01-JUN-2001;
   29-JUN-2001;
  18-JUL-2001;
06-DEC-2001;
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97US-0059113P.
   16-JUL-2001; 2001US-00906646
  (first entry)
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  20-NOV-2003
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   The invention relates to an antibody that binds to a fully defined PRO polypeptide. The antibody is useful for the diagnosis, prevention and/or treatment of disorders associated with the aberrant expression or activity of the PRO polypeptide, such as tumour conditions and cancer. They can also be used to generate transgenic or knockout animals useful in the development and screening of therapeutically useful reagents. The PRO polypeptides and encoding nucleic acids can be used as molecular weight markers for procein electrophoresis, chromosome identification and tissue typing. The antibodies may be used in various diagnostic,
  279
  339
   399
   100
   459
   120
   519
   80
   the
  competitive binding and/or immunoprecipitation assays. The present sequence represents cDNA encoding a human secreted and transmembrane PRO
  40
  9
  GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
  ATCACCCTIGITION
   CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
   TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAAACAGCCTTGAAAGCT
   SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle
   AGCITTGAAACTTGCAGCTATGCCTGGGTTGGAGATGGATTCGTGGTCTCTAGGATT
   SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
   AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
  41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
  WetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu
  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
   Isolated antibody specifically binding a PRO polypeptide, useful for diagnosis and treatment of disorders with the aberrant expression or activity of the PRO polypeptide, such as tumor conditions and cancer.
   Godowski PJ;
   Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
   2372
322
0
0
0
   Goddard A,
Wood WI;
   Conservative:
Mismatches:
   Length:
Matches:
   Indels:
   Gerritsen ME,
Watanabe CK,
   US-10-079-111-1 (1-322) x ACH03578 (1-2372)
   Disclosure, Fig 5, 409pp; English.
  01-MAY-2002; 2002US-00063513
  06-DEC-2001; 2001US-00006867
   1.49e-304
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100.00%
   Filvaroff E,
2, Gurney AL,
  (GETH ) GENENTECH INC
   2003-479475/45.
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Best Local Similarity:
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Grimaldi J
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90
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1059
  1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAAGCAAAACTACCGTGCGATGCCTGGAAGCT 1119
  160
   639
   180
  669
   759
  819
  240
  879
   241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
   939
  280
  300
   320
  Human; gene; ss; PRO; secreted; transmembrane; gastrointestinal mucosa, mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's disease; awyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding anglogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
  200
   220
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SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
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  TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
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  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
   520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
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  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
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  940 AGGTATGTGAAGGCCTTCCCTTTTACAACAAGAATCAGCAGAAGGAAATGATGGAAACC
   LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
   ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle
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  AsplysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla
   Human secreted/transmembrane protein cDNA, #40.
  BP.
  ADA18261 standard; cDNA; 2372
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02-DEC-1999; 99WO-US028564.
16-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030091.
20-DEC-1999; 99WO-US030991.
20-DEC-1999; 99WO-US030991.
11-FEB-2000; 2000WO-US006414.
22-FEB-2000; 2000WO-US00565.
22-FEB-2000; 2000WO-US005641.
20-MAR-2000; 2000WO-US008439.
20-MAR-2000; 2000WO-US014042.
20-MAR-2000; 2000WO-US014042.
22-MAY-2000; 2000WO-US014042.
24-AUG-2000; 2000WO-US01564.
24-AUG-2000; 2000WO-US01564. 18-SEP-2000; 2000US-00665350 

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Godowski PJ, Grimaldi Mather JP, Pan J, Pac Williams PM, Wood WI;

(GETH ) GENENTECH INC.

WPI; 2003-503392/47. P-PSDB; ADA18262.

New secreted and transmembrane polypeptides useful for treating skin, neurodegenerative diseases, asthma, rheumatoid arthritis, psoriasis and multiple sclerosis.

Claim 2; SEQ ID NO 200; 471pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise anthodies that specifically bind to the PRO polypeptides can be used to raise bloadtive molecule to a cell expressing a PRO protypeptides are useful for detecting other properties in a sample and for inking a bloadtive molecule to a cell expressing a PRO polypeptides are useful for detecting other properties are useful for adulating the biological activity of a cell. PRO polypeptides are useful for adulating the biological activity of a cell expressing a PRO polypeptides are also useful for adulating the biological activity of a cell expressing a PRO polypeptides are also useful contracting diseases associated with abnormal keratinocyte (of a cell expressing) pRO polypeptides. PRO polypeptides are also useful diseases associated with abnormal keratinocyte (of gastrointestinal mucosa and the repair of acute and chronic mucosal diseases, amyorrophic lateral sclerosis (ALS), neuropathies and activated propertied as therapeutic targets for anti-tumour furuge, and are also employed therapeutically in vivo for lessening the effects of viral camployed therapeutically in vivo for lessening the effects of viral inferential breating other PRO polypeptides can be also used in assays to determine if it has a role in meurodegenerative diseases or their reversal, as an antitation disease and their portions affect the expression of employed therapeutically in vivo for lessening the effects of viral endometrial bleeding angiogenerative diseases or their reversal, as an antitation may be a role in appotosis. The polymodiceries are useful in concome and gene mapping, in the generating transpent canhais with genetic disorders as which have a role in appotosis. The polymodice the expression of the propertied and for chromosome identification. The processing cherapeutically useful reagents, as probes and for the general parts, as probes and for the general parts of individuals with genet

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9705-0059113P
9705-0059115P
9705-0059112P
9705-0059121P
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9705-005923P
9705-005226F
9705-0062287P
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29-0CT-1997
   1060
  1000
   1120
          940
                                281
   301
  321
   Human
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   120
  160
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  279
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   579
   639
  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
  669
  200
  759
  819
   240
   879
   260
   261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
   SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle 100
   40
  9
  80
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staining and/or assay of sample fluids. Anti-PRO antibodies are useful diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a gene encoding a PRO polynucleotide of the
   GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
  GAAAATAAAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCAGGGTTTG
  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaAlaGlyLeuGlyPheCysTyrValLys
   GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
  ATCACCCTTGTGGGGAAAAAGGCGAAACCAGCTAGAATTTCACAGAAGCTAAGGAGGCC
  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
   TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
   SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
   SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
   GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
   ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle
   CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
  880 CTAGTGCTTGCTCTCTCTTTTTGGTGCTGCAGCTGGATTTTGCTATGTCAAA
   MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu
  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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   520 AGCCGACAGITIGCAGCCTATIGITACAACTCAICIGATACTIGGACTAACTCGIGCAIT
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   U; 0 Other;
   2372
322
0
0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
   .
T
   G; 638
  x ADA18261 (1-2372)
   BP; 721 A; 524 C; 489
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322.00
100.008
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Percent Similarity:
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mammals

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97US-0063738P.
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99US-0146222P.
  99WO-US020944.
  24-FEB-2000; 2000WO-US005004.
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24-FEB-2000;
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   -JUL-1999
  02-DEC-1999;
  20-DEC-1999
  20-DEC-1999;
  -NON-
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### (GETH ) GENENTECH INC.

Ferrara N;
n ME, Goddard A;
Kljavin IJ;
Tumas D; Botstein D, Desnoyers L, Eaton DL, Fong S, Gao W, Gerber H, Gerriteen Grimaldi JC, Gurney AL, Hillan KJ, an J, Paoni NF, Roy MA, Stewart TA, Filvaroti ., Godowski PJ, Grime. "wer JP, Pan J, Paon. Ashkenazi A, Filvaroff E,

WPI; 2003-512316/48. P-PSDB; ABO32791.

New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO1868), useful for treating or diagnosing e.g. cancers, atherosclerosis, infertility, stroke, AIDS or multiple sclerosis in

SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

121

XX.

XX.

XX.

XX.

The invention relates to an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nuclectide encoding any of (a) FRO (secreted and transmembrane protein) polypeptides appearing as AB032756-AB032816, or (b) any of 61 nucleotide sequences having 50-4053bp (c) AB032756-AB032816, or (b) any of 61 nucleotide sequences having 50-4053bp (c) any these 61 nucleotide sequences. Also included are the isolated PRO oplypeptide (lacking its associated signal peptide or an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide or an extracellular comprising the vector comprising the nucleic acid molecule, a host cell peptide), a vector comprising the nucleic acid molecule, a host cell comprising the vector (used to produce the PRO polypeptide), a chimaeric acid molecule comprising the PRO polypeptide fused to a heterologous amino acid sequence, an anti-PRO antibody, detecting PRO245 or PRO1868 polypeptide and modulating any of these PRO polypeptide in a sample suspected of containing any of these PRO polypeptide in a sample suspected of containing any of these PRO polypeptides are useful as pharmaceuticals, diagnostics, biosensors or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for diagnostics, atheroselerosis, infertility, birth defects, premature aging, malignancy (e.g. inflammations, rheumatoid arthritis, psoriasis, multiple sclerosis, atheroselerosis, infertility, birth defects, premature aging, malignancy (e.g. cancers), strokes, heart attacks, hypertension, gastrointestinal ulerations, Parkinson's disease, Alzheimer's disease, or AIDS in mammals. These are also useful for modulating cholesterol uptake in the bolecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for sercening libraries of human colls, generally, particularly for replacing a defective gene. The present the present the present is a cDNA Claim 2; Fig 73; 476pp; English. 

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

2372 322 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: 1.49e-304 322.00 100.00% 100.00% Similarity: Percent Similarity: Alignment Scores: Query Match: Local Best

US-10-079-111-1 (1-322) x ACD66954 (1-2372)

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| 1   | MetAlaArg¢ysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20     |  |
|-----|------------------------------------------------------------------|--|
| 160 |                                                                  |  |
| 21  | ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  |  |
| 220 | GICCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 279 |  |
| 41  | IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  |  |
| 280 | ATCACCCTTGTGAGCAAAAGGCGAACCAGCTGAATTTCACAGAAGCTAAGGAGGCC 339     |  |
| 61  | CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  |  |
| 340 |                                                                  |  |
| 81  | SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle 100 |  |
| 400 | AGCTTTGAAACTTGCAGCTATGCTTGCAGATGCATTCGTGGTCATCTCTAGGATT 459      |  |
| 101 |                                                                  |  |
| 460 | AGCCCAAACCCCAAGTGTGGGGAAAAATGGGGTGGGGTCCTGATTTGGAAGGTTCCAGTG 519 |  |

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1059
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   879
  639
   180
  669
  200
   759
   220
  819
   260
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   280
  940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 999
  281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
   AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCGATACTTGGACTAACTCGTGCATT 579
  ss; gene.
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  CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT
  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
   GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
   ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  1000 AAAGTAGTAAAAGGAGGAGGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAAACT
   GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
  TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
                            ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
   receptor-ligand interaction; cytostatic; chondrocyte; tumour;
   human; PRO; membrane bound protein; membrane bound receptor; cell prolliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor;
  Novel human secreted and transmembrane protein PRO263 cDNA
  ADA19867 standard; cDNA; 2372 BP
   99WO-US005028
99US-00311832
99WO-US010733.
99US-00380137.
99US-00380139.
   2002US-00063567
  20-NOV-2003 (first entry)
   1120 GAAGTT 1125
   GluVal 322
  US2003069394-A1
  02-MAY-2002;
   08-MAR-1999;
14-MAY-1999;
14-MAY-1999;
25-AUG-1999;
25-AUG-1999;
  Homo sapiens
   10-APR-2003.
   30-DEC-1998
  580
  1060
                            141
   161
  640
   181
   700
   820
   880
   261
   301
   321
  201
  260
  221
   241
  RESULT 4:
ADA19867
  qq
  g
  ΩD
   δ
   qq
  ò
  g
  Db
   à
  g
  ò
  ò
  g
   à
   g
  à
   Db
  ò
  à
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and transmembrane proteins. Extracellular proteins play imment for second and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular corganisms. The fate of many individual cells (for example proliferation, migration or adifferentiation) is typically governed by information or received from other cells and the immediate environment. The information of received from transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, cell receptors or membrane bound proteins. These membrane bound proteins can receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention corrections of the invention may have cytostatic activities through the proteins of the invention may have cytostatic activities through the cytomical process of medicanent for challenging or treating as tumour in a mammal. In addition, they may be useful for measuring or the properties of the invention of the invention of a medicament for diagnosing or treating as tumour in a mammal. In addition, they may be useful for measuring or the properties of the invention of a medicament for diagnosing or treating or treating the expression of a tumour associated gene. The present
   This invention relates to novel nucleic acids encoding human PRO secreted
  New isolated PRO polypeptide, useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide, as therapeutic agent e.g. vaccine, and as molecular weight marker.
   sequence is a cDNA sequence which encodes a human PRO protein of the invention.
   PJ;
   Godowski
  T; 0 U; 0 Other;
  2372
322
0
  Goddard A,
Wood WI;
  Length:
Matches:
  BP; 721 A; 524 C; 489 G; 638
   Gerritsen ME,
Watanabe CK,
  Disclosure; Fig 5; 239pp; English.
   1.49e-304
322.00
100.00%
  2000WO-US005841.
   2000US-00644848.
2000WO-US023328.
  2000US-00664610.
   2000WO-US03267B.
  2000WO-US034956.
  2001US-00816744.
   2001US-00854208.
2001US-00854280.
  30-MAY-2001; 2001US-00870574.
  2001US-00869599.
2001US-00908827.
                 99US-00397342.
   2000WO-US005601
  2000WO-US007532.
2000WO-US014042.
  2000WO-US015264
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   2000US-00709238
   2000US-00747259
   2001WO-US006520
   2001WO-US017800
  05-JUN-2001; 2001US-00874503
  06-DEC-2001; 2001US-00006867
   99US-00423844
  2000WO-US030873
   E,
AL,
   (GETH ) GENENTECH INC.
   Filvaroff
   Gurney
   2003-669950/63.
   P-PSDB; ADA19868
  21-MAR 2000;
22-MAY 2000;
22-MAY 2000;
22-AUG-2000;
24-AUG-2000;
18-SEP-2000;
08-NOV-2000;
  Sequence 2372
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15-SEP-1999;
18-CCT-1999;
30-DEC-1999;
18-FEB-2000;
01-MAR-2000;
02-MAR-2000;
   28-FEB-2001;
22-MAR-2001;
   10-MAY-2001;
10-MAY-2001;
  10-NOV-2000;
01-DEC-2000;
  20-DEC-2000;
   20-DEC-2000;
   Grimaldi JC.
   Alignment Scores:
   Eaton
  Pred. No.:
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Conservative:

Percent Similarity:

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  .060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT 1119
  219
  279
  339
  399
   100
   459
  120
  579
   160
  180
  200
  220
   240
   260
  280
   300
  140
  639
   669
   759
  819
   879
   AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
  40
   9
   80
   20
  GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
  340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGAGGACCAAGTTGAAACAGCCTTGAAAGCT
  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArgIle
   GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle
  820 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
  880 CIAGIGCITGCICTCCICTTCTTGGIGCTGCAGCTGGICTTGGAITTTGCIAIGICAA
  261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
   IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
   CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
  400 AGCITIGAAACTIGCAGCIAIGGCIGGIIGGAGAIGGAIICGIGGICAICICIAGGAIT
   460 AGCCCAAACCCCAAGTGTGGGAAAATGGGGTGTGTCCTGATTTGGAAGGTTCCAGTG
  121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCyslle
  ProGlullelleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr
   640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
   CysvalThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
  .000 AAAGTAGTAAAGGAGAGAGAAGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
   SerbroAsnproLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
   760 IGIGICACAGAAGIIIIIAIGGAAACIAGCACCAIGICIACAGAAACIGAACCAIIIIGII
  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
000
Mismatches:
Indels:
Gaps:
                                      (1-2372)
                                     US-10-079-111-1 (1-322) x ADA19867
100.00%
   1120 GAAGIT 1125
   GluVal 322
Local Similarity:
  Н
  21
  41
  141
   241
   301
   61
  101
   181
  201
   81
   161
   221
   321
  281
        Query Match:
DB:
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PRO is a transmembrane protein involved in the formation, differentiation and maintenance of multicellular organisms, and more particularly the proliferation, differentiation and migration of individual cells. The invention describes screening compounds to identify PRO polypeptide agonists and antagonists, anti-PRO antibodies, and immunoconjugates comprising an antibody conjugated to a cytotoxic agent. Specifically, the heterologous protein of the chimeric polypeptide is an epitope tag or an PC region of an immunoglobulin. Through the use of gene therapy, the PRO polypeptide is useful for preparing cytostatic compositions for diagnosing or treating cancer. The polypeptide is also useful as a molecular weight marker for protein electrophoresis purposes. This polypuclectide sequence is a native CDNA clone that encodes human PRO
   219
   21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
   This invention relates to a novel isolated and secreted PRO polypeptide
   gene; PRO; transmembrane; immunoconjugate; cytotoxic; gene therapy;
  160 ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACAGGCTCCTG
   MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu
  Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.
   PJ;
  for
   Godowski
  New PRO nucleic acid, useful for manufacturing a medicament diagnosing or treating tumor or for tissue typing.
  Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
   polypeptide, found in the cDNA library of the invention.
   2337
322
0
0
0
0
  Goddard A,
Wood WI;
  Length:
Matches:
Conservative:
Mismatches:
  Indels:
  άĔ,
  x ADB17250 (1-2372)
   Gerritsen
Watanabe
BP
   Claim 2; Fig 5; 406pp; English.
ADB17250 standard; cDNA; 2372
   10-AUG-1998; 98US-0096012P.
02-UUN-1999; 99WO-US012552.
25-AUG-1999; 99US-01380137.
24-AUG-2000; 2000WO-US02328.
06-DEC-2001; 2001US-00006867.
  2002US-00227693
   1.49e-304
   322.00
100.00%
100.00%
  cytostatic; cancer; human.
  Ē,
  (GETH ) GENENTECH INC.
   Gurney
  Filvaroff
  2003-521821/49.
  US-10-079-111-1 (1-322)
  Percent Similarity:
Best Local Similarity:
  P-PSDB; ADB17251
   US2003050465-A1
   Eaton DL, Fi
Grimaldi JC,
   Homo sapiens.
  26-AUG-2002;
   Alignment Scores:
   20-NOV-2003
  13-MAR-2003
  ADB17250;
  Query Match:
```

```
1059
  339
  399
  100
   459
  120
   519
   140
   579
  160
  639
   180
  669
  200
  759
  220
  819
  240
   879
   260
   939
   280
   999
   300
  320
                                     09
   80
                                  IleThrLeuValSerLyslysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
   ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
   SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal11eSerArg11e
   AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
  AGCCGACAGITITGCAGCCTATIGITACAACTCAICIGATACTIGGACTAACTCGIGCAIT
  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
   CCAGAAATTATCACCACCACAAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA
   GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
  GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle
   CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT
  TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
   GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
  LeuValLeuAlaLeuLeuPheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
   CTAGTGCTTGCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA
  AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATGGAAACC
  retaggeteggactaagttregecegeaaggaceaagtreaaacagectreaaaget
  AGCTTTGAAACTTGCAGCTATGGCTGGATTGGATTCGTGGTCATCTTAGGATT
  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal
  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
   CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
   AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
  AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
   BP
  ACD83115 standard; cDNA; 2372
   (first entry)
  GAAGTT 1125
   GluVal 322
   22-SEP-2003
  340
  1000
  1120
                                    41
  280
   400
  460
   520
   141
   580
  760
   820
  880
   940
  281
   61
   81
  101
   121
  161
  640
  181
  700
   201
   221
  261
   301
   321
  1060
  ACD83115
   45
  RESULT 45
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ID ACD8
XX
AC ACD8
XX
DT 22-S
XX
XX
XX
XX
XX
XX
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XX
XX
           d
  g
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polynucleotide #36

Human PRO

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Human, PRO; gene; ss; secreted polypeptide; transmembrane polypeptide; abnormal bleeding; gynaecological disease; hysterectomy; mucosal lesion; coronary ischaemic condition; gastrointestinal mucosa; skin disease; ALS; keratinocyte differentiation; psoriasis; Parkinson's disease; sathma; Alzheimer's disease; rheumatoid arthritis; multiple sclerosis; cancer; amyotrophic lateral sclerosis; neuropathy; uncontrolled cell growth.
   970S-0059113P
970S-0059113P
970S-0059112P
970S-0059121P
970S-0059122P
970S-0059122P
970S-0059265P
970S-006228F
970S-006228F
970S-006228F
970S-006284P
970S-0063121P
970S-0063121P
970S-0063121P
970S-0063121P
970S-0063124P
970S-0063124P
970S-0063124P
970S-0063128P
970S-0063734P
970S-0063734P
970S-0063734P
970S-0063734P
970S-0063734P
970S-0063734P
970S-0063734P
970S-0064809P
970S-0066120P
970S-0066120P
970S-0066120P
970S-0066120P
970S-0066120P
   98US-0088026P.
   98WO-US018824.
98US-0100262P.
   2001US-00903786
   98WO-US019177
   98WO-US019330
  98US-0100858P
  US2003044793-A1.
   18 SEP 1997

18 SEP 1997

17 OCT 1997

24 OCT 1997

25 OCT 1997

26 OCT 1997

27 OCT 1997

28 OCT 1997

28 OCT 1997

28 OCT 1997

29 OCT 1997

21 OCT 1997

21 OCT 1997

22 OCT 1997

23 OCT 1997

24 OCT 1997

27 OCT 1997

28 OCT 1997

28 OCT 1997

29 OCT 1997

29 OCT 1997

21 OCT 1997

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24 OCT 1997

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25 OCT 1997

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27 OCT 1997

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28 OCT 1997

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21 OCT 1997

22 OCT 1997

23 OCT 1997

24 OCT 1997

27 OCT 1997

27 OCT 1997

28 OCT 1997

27 OCT 1997

28 OCT 1997

27 OCT 1997

28 OC
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07-NOV-1997;
12-NOV-1997;
117-NOV-1997;
118-NOV-1997;
21-NOV-1997;
24-NOV-1997;
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24-NOV-1997;
24-NOV-1997;
25-NOV-1997;
25-NOV-1997;
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10-SEP-1998;
   11-JUL-2001;
   17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
   17-SEP-1997
17-SEP-1997
   16-SEP-1998
  06-MAR-2003
  17-SEP-1997
  SEP-1997
   14-SEP-1998
  Homo
```

0

```
The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polymucleotides encoding them. The PRO polypeptides and polymucleotides can be used in diagnosing or treating abnormal bleeding involved in gynaecological diseases e.g. to avoid or lessen the need for hysterectomy. They can also be used in treating coronary ischaemic conditions, disorders associated with the preservation and maintenance of gastrointestinal aucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis), Parkinson's disease, asthma, rheumatoid arthritis, multiple sclerosis, amyotrophic lateral sclerosis (ALS), neuropathies and diseases related to uncontrolled cell growth, such as cancer. This sequence represents a human PRO polynucleotide of the invention
  Novel secreted and transmembrane PRO polypeptides and polynucleotides encoding them, useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases.
  Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritesen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
  U; 0 Other;
   489 G; 638 T; 0
   Claim 2; Fig 73; 475pp; English.
  721 A; 524 C;
98WO-US019437.
98UG-0104080P.
98WG-0105304P.
98US-0113296P.
99US-0143048P.
99US-0145622P.
99WG-0146222P.
  2000WO-US005004.
2000WO-US005841.
2000WO-US007377.
2000WO-US008439.
  99WO-US020944
  99WO-US021090
99WO-US021547
  2000WO-US003565.
   99WO-US023089
   99WO-US028313
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99WO-US028565
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   99WO-US028214
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  2000WO-US000219
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  (GETH ) GENENTECH INC.
   2003-492256/46.
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  P-PSDB; ABO34851
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02-DEC-1999;
16-DEC-1999;
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30-MAR-2000;
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  02-JUN-2000;
28-JUL-2000;
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17-SEP-1998;
13-OCT-1998;
20-NOV-1998;
01-DEC-1998;
22-DEC-1999;
26-JUL-1999;
26-JUL-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
15-SEP-1999;
15-SEP-1999;
26-OCT-1999;
26-OCT-1999;
  Alignment Scores:
   30-NOV-1999
01-DEC-1999
   Sequence
      8 \times 6 ```

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1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1000 AAAGTAGTAAAAGGAGAGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT 1059
                                                                                                                                                                                                                                                                                                                                                                                        SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160
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                                                                                                         40
                                                                                                                                                                             09
                                                                                                                                                                                                                                                                    TGTAGGCTGCTGGGAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT
                                   MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu
                                                                                                                                                                                                                                                                                                                      SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle
                                                                                                                                                                                                                                                                                                                                        AGCCCAAAACCCCCAAGTGTGGGGAAAAATGGGGTGGTGTCCTGATTTGGAAGGTTCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProGlullelleThrThrIysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAAATAAAGCAGCAGTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCCACGGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuValLeuAlaLeuLeuPheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
                                                                      ATGGCCAGGTGCTTCAGCCTGGTGTTTCTCACTTCCATCTGGACCACGAGGCTCCTG
                                                                                                                                          Greccasecretrinecerecadaacacritrecarecadegererecadearraneced
                                                                                                                                                                             IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
                                                                                                                                                                                                              ATCACCCTTGTGAGGCAAAAGGCGAACCAGCTGAATTTCACAGAAGCTAAGGAGGCC
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                                                                                                       ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
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US-10-079-111-1 (1-322) x ACD83115 (1-2372)
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RESULT

2372 322 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

1.49e-304 322.00 100.00% 100.00%

> Best Local Similarity: Query Match:

Percent Similarity:

Pred. No.:

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tissue typing; immunohistochemical straining; gene therapy; neonatal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoinsulinaemia; hondrocyte; carthitis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritis; anorectic.
                                                                gene; ss; PRO; secreted; transmembrane; therapeutic;
                                                  Human secreted/transmembrane protein cDNA, #40.
       ВР
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9705-0062285P
9705-0063414P
9705-0062814P
9705-00638120P
9705-0063121P
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      ADA16236 standard; cDNA; 2372
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97US-0059117P.
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97US-0059121P.
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97US-0059184P.
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970S-0064809P-
970S-0065846P.
970S-006563AP-
970S-0066120P-
970S-0066136P-
970S-0066453P-
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                                    (first entry)
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103-NOV-1997;
12-NOV-1997;
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18-NOV-1997;
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97US-0066466P.
97US-0066511P.
97US-0066772P.
97US-0066840P.
97US-0068026P.
98US-009803P.
98US-009803P.
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98WO-US019330.
98WG-0100858P.
98US-0104080P.
98US-0103304P.
98US-0113256P.
99US-0143648P.
99US-0145622P.
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2000WO-US015264.
2000WO-US020710.
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#### (GETH ) GENENTECH INC.

Ferrara N; ME, Goddard A; Kljavin IJ; Tumas D; Botstein D, Desnoyers L, Eaton DL, Fong S, Gao W, Gerber H, Gerritsen Grimaldi JC, Gurney AL, Hillan KJ, an J, Paoni NF, Roy MA, Stewart TA, Wood WI; Pan J, Ashkenazi A, Filvaroff E, Godowski PJ, Williams PM, Mather JP,

WPI; 2003-521801/49.

P-PSDB; ADA16237.

New genes encoding for secreted and transmembrane PRO polypeptides, useful for treating e.g. cardiac insufficiency disorders, wounds, cancers, obesity, diabetes, hyperinsulinemia, hypoinsulinemia, or arthritis.

# Claim 2; SEQ ID NO 200; 476pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the mucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protypeptide, for linking a tleast one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides and for inking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity

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RESULT 47
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of a cell expressing PRO polypeptides. The PRO polypeptides or polynucleorides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are useful for stimulating hypertrophy of neonatal conflictions are useful for stimulating hypertrophy of neonatal provideration of endothelial cells, modulating the proliferation of catimulated T-lymphocytes, enhancing the survival or proliferation of catimulated T-lymphocytes, enhancing the survival or proliferation of cells, inducing proliferation and/or receivable metation of chondrocytes. In particular, these are useful for cells, modulating glucose or FRA uptake, inducing proliferation and/or redifferentiation of chondrocytes. In particular, these are useful for detecting or treating cardiac insufficiency disorders, wounds, cancerous tumours, retinal disorders or injuries (e.g. loss of sight due to arthritis pigmentosum), obesity, diabetes, hyperinsulinaemia, or bone or cartilage disorders, wounds, cancerous crethritis) in mammals. PRO polypeptides and their portions affect the arthritis in mammals. PRO polypeptides and their portions affect the expression of genes which have a role in cell death. The polynucleotides are useful in molecular biology including uses as hybridisation probes of or cDNA library to isolate the full-length RRO polypeptides, for generating transgenic and DNA, for preparing PRO polypeptides, for generating transgenic and DNA, for preparing PRO polypeptides, for generating transgenic genetic analysis of individuals with genetic disorders as well as for recombinantly expressing the protein and for chromosome identification. The proteins are useful as molecular marker for protein the effect of the PRO polypeptide (arpagonists). The polymucleotides are useful as molecular marker for protein and proteins are useful as molecular marker for protein securing compounds to identify the RRO polypeptide (arpagonists). The polymucleotides are useful in disquagitic assays for PRO es geneting and protein and protein and protein and protein and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
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Mismatches:
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AGCCGACAGTTTGCAGCCTATTGTTACAACTCCATCTGATACTTGGACTAACTCGTGCATT
                                                                              CCAGAAATTATCACCACAAAGATCCCATATTCAACACTCCAAACTGCAACACAAAACAA
                                                                                                                                                   GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
                                                       ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
                                                                                                                              GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
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                                                                                                                                                                                                                                                                                                          TGTGTCACAGAAGTTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
                                                                                                                                                                                                                                                                                                                                                  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor, receptor-ligand interaction; cytostatic; chondrocyte; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human secreted and transmembrane protein PRO263 cDNA.
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99WO-US010733.
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2000WO-US004341.
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2000WO-US005841.
2000WO-US007532.
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2000WO-US015264.
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2000US-00665350.
2000US-00709238.
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01-UN-2001, 2001US-00870500.
05-UN-2001, 2001US-00874503.
29-UN-2001, 2001US-00868559.
18-UUL-2001, 2001US-00908827.
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2000WO-US032678.
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99US-00397342
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Grimaldi JC, Gurney AL,
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P-PSDB; ADA20040.
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18-OCT-1999;
12-NOV-1999;
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22-AUG-2000;
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28-FEB-2001;
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Godowski PJ; Goddard A, Wood WI; Gerritsen ME, Watanabe CK, New antibody that binds to a secreted protein, designated as PRO polypeptide, useful as pharmaceuticals, diagnostics, biosensors

Disclosure; Fig 5; 235pp; English.

This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information is typically governed by information is often transmitted by secreted polypetides (for example mitogenic is often transmitted by secreted polypetides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences enoved them. The novel provides the amino acid sequences of novel human membrane bound receptors and proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or sequence is a cDNA sequence which encodes a human PRO protein of the

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

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2372	322
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1.49e-304	322.00

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λŏ	21 ValGlnGl	SerLeuArgAl	rile	erCysArglleMetGly 40
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જે દ	61 CysArglet 	euLeuGlyLeuSerLeuAla 	G17L7	SSASpGlnValGluThrAlaLeuLySAla 80
}	81 SerPheG	ThrevsserTvr	ValG	SerArdle 10
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ò	101 SerProAsr	nProLysCysGlyL)	ProAsnProLysCysGlyLysAsnGlyValGlyVal1	
qq	-B	ccccaagrgrggga	AAATGGGGTGGGTGTC	CTGATTTGGAAGGTTCCAGT
ò	121 SerArgGlr	nPheAlaAlaTyrC)	/sTyrAsnSerSerAsp1	ChrTrpThrAsnSerCysIl
Ор	520 AGCCGACAC	AGCCGACAGTTTGCAGCCTATTGTTACAACT	STTACAACTCATCTGAT	CATCTGATACTTGGACTAACTCGTGCATT 579
ò	41	elleThrThrLysAspP 	heAsnThr	r 16
අු	0	TCACCACCAA	CCATATTCAACACT	AAACTGCAACACAAACAACA 63
රු දි	161 GluPheilev	/alSerAspSe 	rThrTyrSerValAlaSerI	ProTyrSerThrIleProAla 180
}	81 ProThr	hrProProAl	, ,	ProArgArgLysLysLeuile 20
g 40	OO CCTACTA	CTACTCCTCCTGCTC	CCAGCTTCCACTTCTATT	CCACGCAGAAAAATTGATT
ò	201 CysValThr	3luValPheMet	GluThrSerThrMetSer	ThrGluThrGluProPheVal 22
qq	-55 -55	SAAGTTTTTATC	GCACCATGTCT	ACAGAAACTGAACCATTTGT
<i>&amp;</i> :	21 GluAs	snLysAlaAlaPheLysAs	ysAsnGluAlaAlaGlyPhe(	4.
Q	20 GAAA	∢;	ğ	CCCACGCTCTG 87
δ	241 LeuValLer	AlaLeuLeuPhe	PheGlyAlaAlaAlaGlyI	
qa	-6	recrererre	GCAGC	recrarercada 93
ò	261 ArgTyrVa]	lLysAlaPheProPhe	neThrAsnLysAsnGlnGlnLysGluMe	tileGluThr 28
qa	rATGT	saacccrrccrr	rtacaaacaagaarcag	AAGGAAATGAT
රු පි	281 Lysvalva]           1000 AAAGTAGT	Lysg ug uLysA               AAGGAGGAGAAGG	laAsnAspSerAsnProAsn( 	ABBGIUGIUSErLyBLySThr 300
Š	A SA	oglugluserf.	S.	ValArgCvsI,enGluAla 32
<b>3</b> 8	i ii	CCCAGAAGAGTCCAAGAG	AGAGTCCAAGCAAACTACCGTG	CGATGCCTGGAAGCT 11:

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The invention relates to an isolated PRO polypeptide. The polypeptide is useful for preparing a composition for diagnosing or treating cancer or for tissue typing. The present sequence represents cDNA encoding a human secreted/transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 IleThrLeuValSeriysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide, useful for preparing a composition for diagnosing grancer or for tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski
                                                                                                                                                                                                            Human secreted/transmembrane polypeptide PRO 263 cDNA
                                                                                                                                                                                                                                                   therapy; cancer; tissue typing; gene
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Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerritsen ME,
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 5; 236pp; English
                                                                                standard; cDNA; 2372 BP
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2000US-00665350
2000US-00709238
2000US-00747259
2000US-00747259
2001US-00806520
2001US-00816744
2001US-00854208
2001US-00854280
2001US-00854280
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99WO-US005028.
99WO-US010132.
99US-00380137.
99US-00380138.
99US-00380142.
99US-00397342.
99US-00403297.
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2000WO-US005841.
2000WO-US00532.
2000WO-US014042.
2000WO-US015264.
2000WO-US015264.
2000WS-US053328.
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2001US-00869599.
2001US-00908827.
2001US-00006867.
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                                                                                                                                                                  (first entry)
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Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
1120 GAAGTT 1125
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P-PSDB; ABO34169.
                                                                                                                                                                                                                                                     ss; gene
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18-OCT-1999;
12-NOV-1999;
30-DEC-1999;
18-FEB-2000;
01-MAR-2000;
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Grimaldi JC,
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14-MAY-1999;
14-MAY-1999;
25-AUG-1999;
25-AUG-1999;
25-AUG-1999;
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                                       RESULT 48
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 $\chi_{2}$   $\chi_{3}$   $\chi_{4}$   $\chi_{5}$   $\chi_{5$ 

140

579

100 459 120 519

219

40

160

639 180 669 200 759 220 260

939

240

879

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Dp  $\delta$ g à

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Novel PRO polypeptides useful for treating Parkinson's disease, Alzheimer's disease, enterocolitis, Zollinger-Ellison syndrome, psoriasis, epidermoid carcinoma of the vulva and gliomas, gynecological
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98WS-0100858P.
98WO-US019437.
98US-0104080P.
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2000WO-US003565.
2000WO-US004414.
2000WO-US005004.
                97US-00643870P.
97US-0064103P.
97US-0064248P.
97US-0065186P.
97US-0065846P.
97US-0065846P.
97US-0065846P.
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970S-006646P.
970S-006671P.
970S-0066770P.
970S-0066840P.
970S-008082EP.
980S-0099803P.
980S-0100262P.
980S-0100262P.
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2000WO-US015264.
2000WO-US020710.
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98US-0113296P.
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99WO-US028564.
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2000WO-US008439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
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Filvaroff E, I
Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JAN-2000; 2
22-FEB-2000; 24-FEB-2000; 24-FEB-2000; 20-MAR-2000; 20-MAR-2000; 30-MAR-2000; 20-MAR-2000; 20-
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10-SEP-1998;
10-SEP-1998;
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16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
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07-NOV-1997;
12-NOV-1997;
17-NOV-1997;
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24-NOV-1997;
24-NOV-1997;
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20-NOV-1998
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21-NOV-1997
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13-SEP-1999
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                       1000 AAAGTAGTAAAAGGAGGAGAAGGCCAATGATGATGAACCTTAATGAGGAATCAAAGAAAACT 1059
                                                                                                              1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGGAAGCT 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gene; ss; PRO; secreted; transmembrane; gastrointestinal mucosa; mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding anglogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
                                                                                    AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted/transmembrane protein cDNA, #40.
                                                                                                                                                                                                                                                                                                                ADA42381 standard; cDNA; 2372 BP.
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9705-0059113P
9705-0059111P
9705-0059121P
9705-0059128P
9705-0059268P
9705-0052285P
9705-0052285P
9705-0062285P
9705-0062128F
9705-006314R
9705-0063121P
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9705-006354P
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                       GAAGTT 1125
                                                                                                                                                                           GluVal 322
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17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
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17-0CT-1997;
21-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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24-0CT-1997;
24-0CT-1997;
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28-OCT-1997
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The polymore around an early an appropriate are useful in molecular biology including uses as hybridisation probes for cond library to isolate the full-length PRO cDNA or to isolate other cDNAs, in the generation of antisense RNA and DNA, for preparing PRO polypeptides, for generating transgenic animals or knockout animals which are useful in the development and screening of therapeutically useful reagents, as probes and for the genetic analysis of individuals with genetic disorders as well as for recombinantly expressing the protein and for chromosome identification. The proteins of individuals with genetic disorders as well as for recombinantly expressing the protein and for chromosome identification. The proteins of therapeutic agents, for screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists) or prevent the effect of the PRO polypeptide (agonists) or prevent the effect of the PRO collypeptide (antagonists) or prevent the effect of the PRO collypeptide (antagonists) or prevent the effect of the PRO collypeptide (antagonists) or prevent the effect of the PRO collypeptide (antagonists) or prevent the effect of the PRO collypeptide (antagonists) or necenting the expression in specific calls in success or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be evention of the protein of the entity of the entity of the protein of the protein of the entity of the entity of the protein of the protein of the entity of differentiation (e.g. psoriated with abnormal keratinory among a sociated with abnormal keratinocyte differentiation (e.g. psoriated with abnormal keratinocyte differentiation (e.g. psoriated), parkinson's disease, Alzheimer's diseases, anyotrophic lateral sclerosis (ALS), neuropathies and additionally, disease related to uncontrolled cell growth, e.g. cancer. PRO polypeptides also serves as tumour specific antigens which may be exploited as therapeutic targets for anti-tumour drugs, and are also employed therapeutically in vivo for lessening the effects of viral infection. The PRO polypeptides can be also used in assays to determine if it has a role in neurodegenerative diseases or their reversal, as an antithrombotic agent with reduced risk for haemorrhage as compared with hepatin, in treating other PRO-associated disorders, in modulating the commercial bleeding angiogenesis, and may also have an effect on kidney tissue. PRO polypeptides and their portions affect the expression of man also have a negletil in a modulating angiogenesis. and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. PRO polypeptides are also useful for treating disorders associated with the preservation and maintenance invention discloses isolated PRO secreted/transmembrane polypeptides Claim 2; SEQ ID NO 200; 479pp; English.

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other; 

MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20 Conservative: Mismatches: Indels: Length: Matches: Gaps: (1-2372)US-10-079-111-1 (1-322) x ADA42381 1.49e-304 322.00 100.00% 100.00% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: ઠે qq

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λ <sub>O</sub>	61 CysArgLeuleuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80 
δ	
셤 :	00 AGCTTTGAAACTTGCAGCTATGGCTTGGAGATGGATTCGTGGTCATCTTAGGATT 45
A 5	101 SELFICABELFOLDSGYPGLYLYBABNGLYVALGIYVALLGULLGUTELYBVALLIFOVAL 120
δλ	ArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 1
q	520 AGCCGACAGITTGCAGCCTATTGTTACAACTCGATACTTGGACTAGGACTAGCATT 579
ନ ପ	141 ProgluileileThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr 160 
ζ	161 GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
q	640 GATITATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACATACTGCC 699
හි සි	181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeulle 200
3 8	01 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluFroPheVal 22
q	-
ò	221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
ор	8
λõ	41 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 26
d d	80 CTAGTGCTTGCTCTCCTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 93
۵ E	261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetileGluThr 280
ò	81 LysValvalLysGluGluLyaAlaAsnAsnSerAsnProAsnGluGluSerLysLysThr 30
: 쥠	00 AAAGTAGTAAAGGAGGAGAAGGCCAATGATGAGCAACCCTAATGAGGAATCAAAGAAAACT 10
ò	rLysThrThrValArgCy
qq	1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGTG
ò	321 GluVal 322
QQ	0 GAAGTT 1
RESU	ULT 50
203	ACD23293 standard; cDNA; 2372 BP.
ξ A S	02329
<b>\$</b> E\$	26-AUG-2003 (first entry)
X E X	Human PRO polynucleotide #36.
KW KW KW	<pre>Human; PRO; gene; ss; Parkinson's disease; Alzheimer's disease; ALS; amyotrophic lateral sclerosis; neuropathy; cancer; viral infection; AIDS; Usher's syndrome; haemorrhage; enterocolitis; Zollinger-Ellison syndrome;</pre>
K K K	
ΚM	atherosclerosis; infertility; birth defect; premature aging; stroke;

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970S-0059113P.
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98US-0109304P.
98WO-US025108.
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diabetic complication.
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              Homo sapiens.
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21-0CT-1997;
24-0CT-1997;
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The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are used for treating diseases related to growth or survival of nerve cells such as Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS) and neuropathies, diseases related to uncontrolled cell growth such as cancer, viral infections, Usher's syndrome, paemorrhage, enterocolitis, cancer, viral infections, usher's syndrome, pastinal ulceration, congenital microvillus atrophy, skin diseases such as psoriasis and epithelial microvillus atrophy, skin diseases such as psoriasis and epithelial cancers, endometrial bleeding, angiogenesis, ischaemic conditions, atherosclerosis, cardiac injury, infertility, birth defects, premature ging, AIDS, stroke and diabetic complications. The polynucleotides are also useful in chromosome and gene mapping. This sequence represents a human PRO polynucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Botstein D, Desnoyers L, Eaton DL, Ferrara N;
Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
Man J, Paoni NF, Roy MA, Stewart TA, Tumas D;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated PRO polypeptides e.g. PRO245 and PRO1868, useful for treating e.g. Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis, cancer, neuropathies, diabetes and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 73; 477pp; English
                                                                                                                                                                                                                                                                05-JAN-2000; 2000WO-US000219.

11-FEB-2000; 2000WO-US005565.

24-FEB-2000; 2000WO-US0056414.

24-FEB-2000; 2000WO-US005604.

02-MAR-2000; 2000WO-US005841.

30-MAR-2000; 2000WO-US007377.

30-MAR-2000; 2000WO-US008439.

22-MAY-2000; 2000WO-US0014439.

02-UUN-2000; 2000WO-US014042.
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99WO-US028214.
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24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
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Mather JP, Pan J,
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29-NOV-1999;
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16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
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                                               08-SEP-1999;
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U; 0 Other;

BP; 721 A; 524 C; 489 G; 638 T; 0

Sequence 2372

Alignment Scores:

Pred. No.:

2332

Length:
Matches:
Conservative:
Mismatches:

1.49e-304 322.00 100.00% 100.00%

Indels:

Best Local Similarity: Query Match:

Percent Similarity:

US-10-079-111-1 (1-322) x ACD23293 (1-2372)

Search completed: September 16, 2004, 02:39:36 Job time : 558 secs Н

- nucleic search, using frame\_plus\_p2n model

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Title: Perfect score:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

seqs, 2523723180 residues

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Word size:

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Xgapext Ygapext Fgapext Delext

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Query Match Length DB Score

Result No.

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                                                                                                                      CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
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US-09-909-320-200
Sequence 200, Application US/09909320
Patent No. US20020132240A1
GENERAL INFORMATION:
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Betsein, David
APPLICANT: Baton, Dan L.
APPLICANT: Ferrari, NappliCANT: Ferrari
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124543A1 3044710CB1 US-10-079-111-2
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Matches:
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Indels:
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US-10-063-569-5

US-10-063-569-5

US-10-063-551-5

US-09-905-348-200

US-09-905-348-200

US-10-063-555-5

US-10-063-554-5

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US-10-079-111-2
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                                                                          280 ATCACCCTTGTGAGCGAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
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       MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu
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Gerber, Hanspeter
Gerritsen, Mary E.
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Query Match:
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Alignment Scores:

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		uleu      CCTG	tGly       GGGG	wAla       GGCC	sAla      AGCT	Argile          AGGATT	Proval         CCAGTG	sile      scarr	rThr      AACA	roAla 	uile      GATT	eVal       TGTT	aLeu       CTG	TLYS	GluThr        GAAACC	SThr       AACT	uGluAla 
		Argle       AGGCT	[]eMe	Lysg]          AGGA	ceuly        TGAA	3.75		er C.	SlnTh	[]ePr       \TACC	CysLe	ProPhev	roThrAlaLeu             cacGGCTCTG	'sTyrvall          scrargro	Ψ	SerLysLysThr 	reugl        TGGA
		rThr 	ysargi]         GCAGAA1	Luala       \AGCT	rala] [     SAGCC	ValileSe	oplys'	rasn(	LaThr        SAACAG	SerThrilePr                   CTACAATACC	rglysi       saaaa	rGlul   -	6	ecys?       TTGC	.uMet]        AATG	uSeri        ATCA	gCys]       sATGC
372		eTrpTh         CTGGA(	erc 	uasnPheThrGluAlaLysGluA 	YLysAspGlnValGluThrAlaLeuLysAl. 	valva 	1GlyValLeuIleTrpLysVa 	erAspThrTrpThrAsnS                 crgatactrgGacraacr	GlnThralaThrGlnThrThr 	SerProTyrSe	ArgA:	erThrGluThrGluP. 	GlyvalE          GGTGTCC	aGlyLeuGlyPheCy                    GGTCTTGGATTTTG	Lysg] 	roAsnGluGluSe 	vala      grece
e:	(2)	eril 	GlnValSe            CAGGTGTC	SnPhe       ATTTC	lnva]        AAGTT	spGlyPheValV            \TGGATTCGTGG	aller        rccro	SpTh:	hrglr 	erPro	lePro 	erThi 	hegly        TTGG2	lyter        GICTI	inglr       AGCAG	ProAsn 	hrThr        CTACC
71. 98:	(1-237	uThrs        CACTT		nLeuz       GCTG	saspo        GGACO	GlyAspG           GGAGATG	161 yv 	rSerA         ATCTG	eAsnT        CAACA	1Alas        GGCAT	rSer1	rMets        CATGI	laAlaGlyPheGlyGly 	laalaalaG           CTGCAGCTG	sAsnG       GAATC	rasn       aac	rLysT        CAAAA
Length: Matches: Conserva! Mismatche Indels: Gaps:	200	Leule 	LeuSerIle          GCTTTCCATO	anginginieu            \ccAgcAgcTG	Glyby 	rpvalG1          GGGTTGC	G1yVa         GGGGT	AsnSe         AACTC	ilePh         ATATI	Serva         TCGGT	SerTh 	SerTh       AGCAC	AlaAl       GCTGC	AlaAl        GCTGC	roPheThrasnLysasnGlnGlnLysGluMetll 	Aspse       GATAG	rlysSerProSerlysThrThrValArgCysLe 
Lenc Mato Con Miss Inde	088B-	alleu       rGTTG	NaGluGluLe           SCAGAAGAGCT	rsAlaAsn          IGGCGAAC	euAla       TGGCC	lyTrp [[[]] GCTGG	ysasn       aaaat	ystyr       GTTAC	SpPro        ATCCC	hrTyr        ccrac	roala        CAGCT	luThr       AAACT	rsAsnGluAla            \GAATGAAGCT	nePheGlyAla              CTTTGGTGCT	heThr        TTACA	luLysalaasnasp                  \GAAGGCCAATGAT	ysser       AGAGT
	-606-	rleuV        CCTGG	gAlaG        TGCAG	rLysLysA           scaaaaagg	uSerL       AAGTT	rTyrGlyTr           cTATGGCTG	BG1yL        TGGGA	aTyrc        CTATT	rLysa        caaag	pSerT       CAGTA	oAlaP       TGCTC	eMetG       TATGG	eLysa        aaaga	uLeuPheP          ccrcrrcr		uLysa       3AAGG	uSerL  - - - GTCCA
2.00 0.00 0.00 0.00 0.00	US-09	Phese       TTCAG	rLeuArgA] 	1SerLy        GAGCAA	uteuGlyteuSerteuAlaGl; 	eGluThrCysser               GAACTTGCAGC	olyscysglylysasnglyva 	ArgGlnPheAlaAlaTyrCysTyrAsnSerS 	roGluileileThrThrLysAspProilePheAsnThr 		roThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 	GluValPheMetGluThrSerThrMetS 	GluAsnLysAlaAlaPheLy: 	Leule	AlaPhe        GCCTTCC	alLysGluGlu            :AAAGGAGGAG	roglugluser            ccagaagagro
330	x (2	rgCys        3GTGC	lyser        GCTCT	euVa      rrgr	euleu        rgcrg	luThr        AAACT	roasnPro	InPhe       AGTTT	leile        TATC	leval        TGTC	orThr          aracr	orglu        agaa	sala      	albeuAlabeu 	allysala           rGaaggcc	allys(       FAAAG	snPro       ACCCA
ty: arity	(1-32	talaa       GGCCA	161nG        CCAAG	eThrie         cacccr	sArglet         rAGGCTC	rPheG        criig		SerargG         aGCCGAC	ogluI       AGAAA	GluPhel          GAATTTA	OThrT]        FACTA	ysvalThro	Ashli 	euValli       TAGTGC	TYrva        STATGT	sValVa]        \GTAGTZ	pLysasnPr           \TaaaaaCCC
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Pred. No Score: Percent Best Loc Query Ma	-10-0																
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NOS: 423
                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                   Best Local Similarity:
Query Match:
    NUMBER OF SEQ ID
                                                                                                                                                                                Score:
Percent Similarity:
                                                                                                  US-09-905-291A-200
                                                                                                                                         Alignment Scores:
Pred. No.:
                  SEQ ID NO 200
LENGTH: 2372
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/905,291A

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PRIOR PELLING DATE: 1999-01-15

PRIOR PELLING DATE: 1999-01-15

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                                                                                                            Sequence 200, Application US/09905291A
Patent No. US20020160374A1
GENERAL INFORMATION:
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APPLICANT: Forgo, Ellen
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APPLICANT: Gao, Wei-Qiang
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
                                                                                                                                                                                                                                                                                                                                                    Gerber, Hanspeter
Gerritsen, Mary E
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                                    1120 GAAGTT 1125
GluVal 322
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  Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR PPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 200
LENGTH: 2372
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APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Rey, Margaret Ann
APPLICANT: Pan, James
APPLICANT: Tunas, Daniel
APPLICANT: Tunas, Daniel
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Milliams, P. Mickey
APPLICANT: Milliams, P. Mickey
APPLICANT: Modod, William, I.
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT APPLICATION NUMBER: US/09/665,350
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-26
PRIOR FILING DATE: 1999-09-36
PRIOR PLING DATE: 1999-09-19
PRIOR PLING DATE: 1999-09-19
PRIOR APPLICATION NUMBER: PCT/US99/2034
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/2814
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
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       LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
                               1000 AAAGTAGTAAAGGAGAAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGT
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Publication No. US20020192659A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bakkenazi, Avi
APPLICANT: Bestein, David
APPLICANT: Eaton, David
APPLICANT: Eaton, Dan L
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Gerritsen, Mary E.
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US-09-907-824-200
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Best Local Similarity:
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                      AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
                                                                      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
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APPLICANT: GLIMAID, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Mathar, Johnie P.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane F.
IITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 104-66-14
CURRENT APPLICATION NUMBER: US/09/907,824
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PRIOR PELING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 99/665,350
PRIOR APPLICATION NUMBER: 90/143,048
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR PAPLICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
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Publication No. US20020197671A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Goddard, A.
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Matches:
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
PURCHARLE SEQ ID NOS: 423
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81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArglle 100
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PPLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LENGTH: 2372
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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-01-20
PRIOR FILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: US 60/146,222
PRIOR FILING DATE: US 60/146,222
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                                                                                     760 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
                                                                                                                               GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
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                                            201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
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Grimaldi, Christopher
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Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Betsein, David
APPLICANT: Betstein, David
APPLICANT: Eaton, Da L.
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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Hillan, Kenneth, J
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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APPLICANT: Garmacla, Christopher J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pach, James
APPLICANT: Pach, Margaret Ann
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, I.
TILLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION NUMBER: US/09/904,011
CURRENT APPLICATION NUMBER: 2001-07-11
PRIOR PELICATION NUMBER: PCT/US00/04414
CURRENT APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US CIVESOP/20594
PRIOR APPLICATION NUMBER: US FOT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
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                  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
                                                                          880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCTGGTCTTGGTTTTTGCTATGTCAAA 939
                                                                                                                    261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 200, Application US/09904011
Publication No. US20030003530A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
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Godowski, Paul J.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin I.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Gao, Sherman
Gao, Wei-Qiang
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APPLICANT:
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PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
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US-09-904-011-200
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
ProThrThrThrProProAlaProAlaSerThrSerIleProArghrgLysLysLeuile
                                                                 700 CCTACTACTCCTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGGAGAAAAAATTGATT
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                                                                                                         CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
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Grimaldi, Christopher
Gurney, Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Botstein, David
Desnoyers, Luc
Eaton, Dan I.
Ferrara, Napoleone
Filvaroff, Ellen
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Gao, Wel-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, Davi
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Matches:
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,048
PRIOR PLING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21597
PRIOR PILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30995
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PLING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PRIOR DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PRIOR DATE: 1990-0-12-06
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US99/30999
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ORGANISM: Homo Sapien
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CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
APPLICANT: Wood, William, I. IIILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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                                                   THILE OF INVENTION: ACIDE ELICOLLING LIE DAMING
CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIOR PLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2000-09-18
PRIOR PLING DATE: 2000-02-22
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-09-13
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PRIOR PLING DATE: 1999-10-05
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Query Match:
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ORGANISM: Homo
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                      AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
                                                                                                         GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
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  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J
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Gerritsen, Mary E.
Goddard, A.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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                                                                                           APPLICANT: Aljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Paoni, Micholas F.
APPLICANT: Paoni, Micholas F.
APPLICANT: Paoni, Micholas F.
APPLICANT: Paoni, Micholas F.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, P. Mickey
APPLICANT: Wolliams, Daniel
CURRENT APPLICATION NUMBER: US/09/907,613
FILING OF INVENTION: Secreted and Transmembrane F. FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
PRIOR FILING DATE: 1099-00-07
PRIOR FILING DATE: 1999-00-07
PRIOR FILING DATE: 1999-00-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-11-30
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                                          Gurney, Austin L.
Hillan, Kenneth,
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                      Sequence 200, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bathkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Betsein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Fatrara, Napoleone
APPLICANT: Filvaroff, Blen
APPLICANT: Following Applicant: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following APPLICANT: Following AP
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Gerritsen, Mary E.
Goddard, A.
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Grimaldi, Christopher
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Hillan, Kenneth, J
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Gerritsen, Mary E.
                               Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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               Ferrara,
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Percent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT:
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IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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; APPLICANT: Genentech, Inc.; APPLICANT: Ashkenazi, Avi; APPLICANT: Besteein, David; APPLICANT: Besteein, David; APPLICANT: Eaton, Dan L.
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Sequence 200, Application US/09904859
Publication No. US20030036060A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                            Ferrara, Napoleone
Filvaroff, Ellen
                                              Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                               Goddard, A.
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                                                                                                                              41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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                                     1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu
              US-10-079-111-1 (1-322) x US-09-907-942-200 (1-2372)
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APPLICANT: Hillah, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TILLE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/909,204

CURRENT PILLIGN DATE: 2001-07-18

PRIOR APPLICATION NUMBER: US/09/909,204

PRIOR APPLICATION NUMBER: PCT/USO0/04414

PRIOR FILLING DATE: 1999-07-05

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PRIOR FILLING DATE: 1999-09-13

PRIOR FILLING DATE: 1999-09-15

PRIOR FILLING DATE: 1999-09-15

PRIOR FILLING DATE: 1999-09-15

PRIOR PRIOR DATE: 1999-09-15

PRIOR PRIOR DATE: 1999-09-15

PRIOR PRIOR DATE: 1999-10-15

PRIOR PRIOR DATE: 1999-10-15

PRIOR PRILING DATE: 1999-10-15

PRIOR PRILING DATE: 1999-11-29

PRIOR PRILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28564

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PRIOR PRILING DATE: 1999-11-29

PRIOR PRILING DATE: 1999-11-30

PRIOR PRILING DATE: 1999-11-30

PRIOR PRILING DATE: 1999-11-30

PRIOR PRILING DATE: 1999-12-02

PRIOR PRILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR PRILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

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PRIOR PRILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

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PRIOR PRILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR PRILING DATE: 1999-12-02
                                                                                                                                                                        Sequence 200, Application US/09909204
Publication No. US20030036061A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Askhenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Filvaroff, Ellen
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Gerritsen, Mary E.
Goddard, A.
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Eaton, Dan L.
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Mismatches:
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Matches:
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; ORGANISM: Homo Sapien
US-09-904-859-200
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Best Local Similarity:
Query Match:
DB:
                                                 Alignment Scores:
Pred. No.:
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1000 AAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGAAAAT 1059
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APPLICANT: Hilan, Kenneth, J.
APPLICANT: Hilan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
                               940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATGAAACC
  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
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CURRENT APPLICATION NUMBER: US/09/904,820

CURRENT FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-22

PRIOR PLICATION NUMBER: US 60/143,048

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PILING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-09-19

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-15

PRIOR FLING DATE: 1999-09-15

PRIOR FLING DATE: 1999-09-15

PRIOR FLING DATE: 1999-10-15
                                                                                                                                                                                                                                                                                                                                                                Sequence 200, Application US/09904820 Publication No. US20030036094A1 GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 200
LENGTH: 2372
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CNGANISM: Homo sapiens
US-09-909-204-200
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241 LeuValLeuAlaLeuLeuPhePheG]yAlaAlaAlaG]yLeuG]yPheCysTyrValLys 260
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APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,786
                                                                                                                                                                                                                                                                                                          301 AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
          760 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
                                                                        820 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
                                                                                                                          880 CTAGTGCTTGCTCTCTTCTTTGGTGCTGCTGGTCTTGGATTTTGCTATAAA
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                                           GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
                                                                                                                                                                          ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
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Matches:
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Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 200, Application US/09904786; Publication No. US20030039969A1; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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ORGANISM: Homo Sapien
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Matches:
PRIOR APPLICATION NUMBER: PCT/US99/28113
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR PAPLICATION NUMBER: PCT/US99/3091
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-0
PRIOR FILING DATE: 1999-12-0
PRIOR PILING DATE: 1999-12-0
PRIOR PILING DATE: 1999-12-0
PRIOR PILING DATE: 2090-01-05
NUMBER OF SEQ ID NOS: 423
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; ORGANISM: Homo Sapien
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembran
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US/09/906,646
PRIOR APPLICATION NUMBER: PCT/USO/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
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PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-12-07
                                                                                                              ; Sequence 200, Application US/09906646; Publication No. US20030039971A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski, Paul J.
Grimaldi, Christopher
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Hillan, Kenneth, J.
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Gerritsen, Mary E.
Goddard, A.
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
   1120 GAAGTT 1125
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   Conservative:
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                              Mismatches:
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   Percent Similarity:
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                                               1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT 1119
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                                                                                                                                       Sequence 200, Application US/09906700; Publication No. US20030039972A1; GENERAL INPORMATION:
APPLICANT: Genentech, Inc.; APPLICANT: Botstein, David; APPLICANT: Besnoyers, Luc; APPLICANT: Eaton, Dan I.; APPLICANT: Ferrara, Napoleone; APPLICANT: Filvarofff, Ellen;
                                                                                                                                                                                                                                                                                                            Goddard, A. Godowski, Paul J. Godowski, Paul J. Grimaldi, Christopher J. Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Wood, William, I.
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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                                                                                Matches:
Conservative:
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Indels:
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         TYPE: DNA
CORGANISM: Homo sapiens
US-09-906-646-200
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Query Match:
DB:
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Pred. No.:
LENGTH: 2372
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, Jimes
APPLICANT: Pon, Margaret Ann
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
                                                                                  940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATGAACC
                                                                                                                                             281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
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                                                    ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
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CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/06/5,350
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR PLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PELING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 200, Application US/09903786 Publication No. US20030044793A1 GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR PELLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 200
LENGTH: 2372
TYPE: DNA
PRIOR HOMO SADIENS
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,903
CURRENT PLING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 1900-0-2-2
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR FILING DATE: POPPLOATON NUMBER: US 60/146,222
PRIOR FILING DATE: PCT/US99/20594
PRIOR FILING DATE: PCT/US99/20594
                                                                                                                                                             LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
                                                                               GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
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         CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                               TGTGTCACAGAAACTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
                                                                                                                     820 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCCACGGCTCTG
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Besterin, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-0
PRIOR PLING DATE: 1999-12-0
PRIOR PLING DATE: 1999-12-0
PRIOR PLING DATE: 1999-12-0
PRIOR FILING DATE: 1999-12-0
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ORGANISM: Homo Sapien
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Best Local Similarity:
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DB:
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US-09-903-786-200
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2372
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                    GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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                                                640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Ashkenazi, Avi
APPLICANT: Betstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-15
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CRGANISM: Homo sapiens
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
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PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
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PRIOR PELING DATE: 2009-15
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PRIOR PELING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 423
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US-09-903-749A-200
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     340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
                                                     SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
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                                                                                                         400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTTAGGATT
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Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Bestein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Faton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                           TILLE REPERBRUCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904,119

CURRENT APPLICATION NUMBER: US/09/904,119

CURRENT FILING DATE: 2001-07-11

PRIOR PELING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-09-18

PRIOR PLING DATE: 1999-09-18

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PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-20

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1999-12-06

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                                                                                 280 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
                                      IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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                                                                                                                            CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
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; APPLICANT: Genentech, Inc.; APPLICANT: Ashkenazi, Avi; APPLICANT: Desnoyers, Luc; APPLICANT: Eacon, Dan L.; APPLICANT: Ferrara, Napoleone
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                                                                 APPLICANT: Machine P.
APPLICANT: Machine P.
APPLICANT: Pan, James
APPLICANT: Mod, Walliams, P. Mickey
TITLE OF INVENTION: Accreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Accreted and Transmembrane Polypeptides and Nucleic
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FRIGHT FILING DATE: 2001-07-12
FRIGHT FILING DATE: 1000-02-22
FRIGHT PELING DATE: 1000-02-22
FRIGHT PELING DATE: 1000-07-22
FRIGHT PELING DATE: 1000-07-23
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             Hillan, Kenneth, .
Kljavin, Ivar J.
Mather, Jennie P.
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; ORGANISM: HOMO
US-09-904-956-200
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                                          US-10-079-111-1 (1-322) x US-09-902-736-200 (1-2372)
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
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Matches:
Conservative:
Mismatches:
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PRIOR PELING DATE: 2000-09-18
PRIOR PELING DATE: 2000-09-18
PRIOR PELING DATE: 2000-09-18
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-20
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PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-03
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                                                                                                                              Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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ORGANISM: Homo Sapien
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Best Local Similarity:
Query Match:
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LENGTH: 2372
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     ) ORGANISM: Homo Sapien
US-09-907-794-200
                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                           Alignment Scores:
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, I.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794
CURRENT APPLICATION NUMBER: US/09/907,794
CURRENT APPLICATION NUMBER: US 60/145,698
REIOR PILING DATE: 2000-02-22
REIOR APPLICATION NUMBER: US 60/145,698
REIOR FILING DATE: 1999-07-05
PRIOR APPLICATION NUMBER: US 60/145,698
REIOR FILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: US 60/145,698
REIOR RILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: US 60/145,698
REIOR RILING DATE: 1999-07-18
PRIOR APPLICATION NUMBER: PCT/US99/20309
PRIOR APPLICATION NUMBER: PCT/US99/20309
PRIOR APPLICATION NUMBER: PCT/US99/20309
PRIOR APPLICATION NUMBER: PCT/US99/20313
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/2091
PRIOR PILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR PILING DATE: 1999-12-0
PRIOR PILING DATE: 1999-12-0
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR PILING DATE: 1999-12-0
PRIOR PILING DATE: 1999-13-0
PRIOR PILING DATE: 1999-13-0
PRIOR PILING DATE: 1999-13-0
PRIOR PILING DAT
Sequence 200, Application US/09907794
Publication No. US20030049677A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Destochi, David
APPLICANT: Eston, David
APPLICANT: Eston, David
                                                                                                                                                                                                                                                                         Godowski, Paul J.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniell,
                                                                                                                                                 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Goddard, A.
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                                                                                                                                                                                                                                                                                                                                               41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArglle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValyValProThrAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
Length:
Matches:
Conservative:
Mismatches:
Indels:
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GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 AGCCCAAACCCCCAAGTGTGGGAAAAATGGGGTGTGCTGGTTTTGGAAGGTTCCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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ORGANISM: Homo Sapien
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Best Local Similarity:
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                                                       1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT 1119
                        AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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APPLICANT: Wood, William, I.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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CURRENT PILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/665,350
PRIOR FILING DATE: 2000-00-18
PRIOR FILING DATE: 2000-00-18
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-18
PRIOR PILING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28014
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28114
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
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Grimaldi, Christopher J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferrara, Napoleone
Filvaroff, Ellen
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Paoni, Nicholas F.
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                        APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Dan L.
APPLICANT: Eaton, Dan L.
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                                                                                                               GluVal 322
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US-09-903-943-200
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PRIOR FILING DATE: 1999-10 FRIOR APPLICATION NUMBER: FRIOR TILING DATE: 1999-11 FRIOR FILING DATE: 1999-11 FRIOR FILING DATE: 1999-12 FRIOR FILING DATE: 1999-12 FRIOR PRIOR FILING DATE: 1999-12 FRIOR FILING DATE: 1999-12	PRIOR FILING DATE: 1999-12 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-01 NUMBER OF SEQ ID NOS: 423 SEQ ID NO 200 IENGTH: 2372 TYPE: DNA OSGANISM: HOMO Sapien US-09-904-462-200	Alignment Scores:  Pred. No.:  Score:  Percent Similarity:  Best Local Similarity:  100.0  Query Match:  10.0  DB:	US-10-079-111-1 (1-322) x US- QY 1 MetAlaArgCysPhe: 	Oy 21 ValGlnGlySerLew	Oy 61 CysargleuLeuGly/	Oy 101 SerProAsnProLyse	Oy 141 ProGluIleIleThrT
	Gluval 322           GAAGTT 1125 2-200 00, Application US/09904462	GENERAL INCERMENTION:   APPLICANT: Genentech, Inc.   APPLICANT: Ashkenazi, Avi   APPLICANT: Botstein, David   APPLICANT: Besnoyers, Luc   APPLICANT: Eaton, Dan L.   APPLICANT: Ferrara, Napoleone   APPLICANT: Filvaroff, Ellen   APPLICANT: Ford cherment	APPLICANT: Gao, Wel-Qiang APPLICANT: Gacher, Hanspeter APPLICANT: Gerber, Hanspeter APPLICANT: Gerritsen, Mary E. APPLICANT: Godowski, Paul APPLICANT: Godowski, Paul	APPLICANT: GITMBIO, UNISCOPNET J. APPLICANT: GUTNBY AUSTIN L. APPLICANT: Hillan, Kenneth, J. APPLICANT: Midher, Jennie P. APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Pan, Margaret Ann APPLICANT: Pan, Margaret Ann APPLICANT: Pan, Margaret Ann	## APPLICANT: Tunmas, Daniel   APPLICANT: Tunmas, Daniel   APPLICANT: Tunmas, Daniel   APPLICANT: Williams, P. Mickey   APPLICANT: Williams, I.   TILLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic   TITLE OF INVENTION: Acids Encoding the Same   FILE REFERENCE: 10466-14   CURRENT APPLICATION NUMBER: US/09/904,462   CURRENT FILING DATE: 2001-07-13	PRIOR APPLICATION NUMBER: 09/665,350	FRIOR FILING DATE: 1999-07-26  PRIOR FILING DATE: 1999-07-28  PRIOR APPLICATION NUMBER: DCT/US99/20594  PRIOR APLICATION NUMBER: PCT/US99/20594  PRIOR FILING DATE: 1999-09-08  PRIOR PILING DATE: 1999-09-13  PRIOR APLICATION NUMBER: PCT/US99/21090  PRIOR APPLICATION NUMBER: PCT/US99/21090  PRIOR APPLICATION NUMBER: PCT/US99/21547  PRIOR APPLICATION NUMBER: PCT/US99/21547  PRIOR FILING DATE: 1999-09-15  PRIOR PILING DATE: 1999-09-15  PRIOR APPLICATION NUMBER: PCT/US99/23089

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eSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
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Matches:
Conservative:
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Gaps:
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CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                                TGTGTCACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT
                                                                                       GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane F.
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBNCE: 10466-118
CURRENT APPLICATION NUMBER: US/09/907,925
CURRENT FILING DATE: 2001-07-17
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
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US-09-907-925-200
Sequence 200, Application US/09907925
Publication No. US20030054352A1
GENERAL INFERMATION:
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Godowski, Paul J.
Grimaldi, Christopher
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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APPLICANT Shkenazi, Avi
APPLICANT Botstein, David
APPLICANT Besnoyers, Luc
APPLICANT Exton, Dan L.
APPLICANT Ferrara, Napoleone
APPLICANT Filvaroff, Bilen
APPLICANT Filvaroff, Bilen
APPLICANT Gao, Wei-Qiang
APPLICANT Gao, Wei-Qiang
APPLICANT Gerber, Hanspeter
APPLICANT Gerber, Hanspeter
APPLICANT Gerritsen, Mary E.
APPLICANT Godward, A.
APPLICANT Grimaldi, Christop
APPLICANT Grimaldi, Ivar J.
APPLICANT David James
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Mather, Jennie P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG
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Matches:
PRIOR FILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILICATION NUMBER: PCT/US99/20544
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30991
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Best Local Similarity:
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TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-902-692-200
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Pred. No.:
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                                                                                                                  CCTACTACTACTCCCCCCCCCCCCCCCTCCCACTTCTATTCCACGAGAAAAAATTGATT
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,692
                GAATITATIGICAGIGACAGIACCIACICGGIGGCAICCCCIIACICIACAAIACCIGCC
                                                                                                  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle
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                                          GluPheIleValSerAspSerThrTyrSerValAlaSerProfyrSerThrIleProAla
US-09-902-692-200
Sequence 200, Application US/09902692
Publication No. US20030054400A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
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Botstein, David
Desnoyers, Iuc
Eaton, Dan I.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Mather, Jennie P.
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Matches:
CURRENT FILLING DATE: 2000-02-22
PRIOR PELICATION NUMBER: PCT/USOU/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: BCT/USOU/0419, 048
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
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PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-12-02
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PRIOR PILING DATE: 1999-12-07
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ORGANISM: Homo Sapien
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Best Local Similarity:
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  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCys1le
                                                      141 ProGluilelleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr
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US-09-903-520-200
; Sequence 200, Application US/09903520
; Publication No. US20030054401A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Bathenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Besnoyers, Luc
; APPLICANT: Eaton, Dan I.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Filvaroff, Ellen
Fong, Sherman
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Paoni, Nicholas F.
Roy, Margaret Ann
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Indels:
         Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillain, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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US-09-905-056-200
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                               340 TGTAGGCTGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAAACGT
                                                               SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
                                                                                                                                            AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
                                                                                                                                                                     SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
                                                                                                                                                                                  640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
              CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
                                                                                        400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTTAGGATT
                                                                                                                  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal
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Publication No. US20030054441A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bathenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Good, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
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US-09-905-056-200
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Matches:
Conservative:
Mismatches:
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembran
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/909,064

CURRENT FILING DATE: 2001-07-18

PRIOR PILING DATE: 2001-07-22

PRIOR PILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-06

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 19
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                                                                                                                                                                            Godowski, Paul J.
Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Williams, P. Mickey
Wood, William, I.
                                                                  Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Roy, Margaret Ann
Stewart, Timothy A.
                            Ferrara, Napoleone
Filvaroff, Ellen
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           Eaton, Dan L.
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ORGANISM: Homo sapiens
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Best Local Similarity:
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                                                                                                                                                                                                                                                          SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile 100
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ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
                               220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
                                                                                    41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
                                                                                                                                                                      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
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US-09-909-064-200
US-09-909-064-200
; Sequence 200, Application US/0990964
; Publication No. US20030059772A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
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APPLICANT: Williams, Danie,
APPLICANT: Williams, Danie,
APPLICANT: Williams, Danie,
APPLICANT: Wood, William:
TITLE OF INVENTON: Acids Encoding the Same
TITLE OF INVENTON: Acids Encoding the Same
TITLE OF INVENTON: Acids Encoding the Same
TITLE REPRENDICE: 1046-61-01-22
CURRENT FILING DATE: 2000-01-22
CURRENT FILING DATE: 1090-07-01-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-36
PRIOR PELING DATE: 1999-07-36
PRIOR PELING DATE: 1999-07-36
PRIOR PELING DATE: 1999-07-36
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
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PRIOR PELING DATE: 1999-10-14
PRIOR PELING DATE: 1999-10-15
PRIOR PELING DATE: 1999-10-15
PRIOR PELING DATE: 1999-10-15
PRIOR PELING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/US99/2813
PRIOR PELING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28014
PRIOR APPLICATION NUMBER: PCT/US99/28016
PRIOR APPLICATION NUMBER: PCT/US99/28016
PRIOR APPLICATION NUMBER: PCT/US99/28091
PRIOR APPLICATION NUMBER: PCT/US99/28099
PRIOR PELING DATE: 1999-12-20
PRIOR PELING 
                  US-09-904-553-200
; Sequence 200, Application US/09904553
; Publication No. US20030059828A1
; GENERAL INFORMATION:
; APPLICANT: Genemtech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Rijavin, Ivar J.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA 639
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Scoreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/065,381
RIOR APPLICATION NUMBER: US/06/65,350
RRIOR FILING DATE: 2000-09-18
RRIOR FILING DATE: 2000-09-18
RRIOR FILING DATE: 1999-07-26
RRIOR FILING DATE: 1999-07-26
RRIOR FILING DATE: 1999-07-26
RRIOR FILING DATE: 1999-09-07-26
RRIOR FILING DATE: 1999-09-15
RRIOR FILING DATE: 1999-10-00
RRIOR RELIGATION NUMBER: PCT/US99/28564
RRIOR RFLING DATE: 1999-12-00
RRIOR FILING DATE: 1999-12-00
RRIOR FILING DATE: 1999-12-00
RRIOR FILING DATE: 1999-12-00
RRIOR FILING DATE: 1999-12-00
       301 AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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Grimaldi, Christopher
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E
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Botstein, David
Desnoyers, Luc
Eaton, Dan L
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, Davi
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Matches:
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US-09-904-553-200
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Query Match:
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     880 CTAGTGCTTGCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTTGCTATGTCAAA 939
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APPLICANT: Hillan, Kenneth, J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Milan, Kenneth, J.
APPLICANT: Mather, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Poy, Margaret Ann
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, I.
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APPLICANT: Wood, Milliam, I.
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APPLICANT: Mood, Milliam, II
APPLICANT: Milliam, II
APPLICAN
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                                                                                                                                                         281 LysvalvalLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
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                                                ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
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CURRENT PELLING DATE: 2001-07-12
PRIOR PELLING DATE: 2001-07-12
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PRIOR PILING DATE: 2000-00-18
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PRIOR PELLING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/23089
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Grimaldi, Christopher
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
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Botstein, David
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PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
LENGTH: 2372
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        CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                                 GluAsnIysAlaAlaPheIysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
                                                                                                                 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGCGTTTTGGAGGTGTCCCCCACGGCTCTG
                                                                                                                                                                                                         CTAGTGCTTGCTCCTCTTTTGGTGCTGCTGGTCTTGGATTTTGCTATGTCAAA
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR PLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
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Grimaldi, Christopher J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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E, Ellen
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Botstein, David
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Eaton, Dan L.
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Filvaroff,
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              PRIOR FILING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

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PRIOR FILING DATE: 1999-11-30

PRIOR PLING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/3099

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1999-12-16

PRIOR PLING DATE: 1999-12-16

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 200
APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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Best Local Similarity:
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      ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuile
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,075
CURRENT FILING DATE: 2001-07-13
Prior application data removed. Check file wrap
NUMBER OF SEQ ID NOS: 423
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; Sequence 200, Application US/09905075
; Publication No. US20030077583A1
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Garritsen, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Goddwski, Paul J.
Grimaldi, Christopher J.
Grimaldi, Christopher J.
Grimaldi, Christopher J.
Kijavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Genentech, Inc.
APPLICANT: Bathkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Inc.
APPLICANT: Eaton, Dan L.
APPLICANT: Fitvaroff, Englene
APPLICANT: Fitvaroff, Elenene
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PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

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PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-16

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1999-12-06

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PRIOR FILING DATE: 1999-12-20

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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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US-09-907-575-200
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APPLICANT: Tunas, Dania APPLICANT: Tunas, Dania APPLICANT: Tunas, Dania APPLICANT: Tunas, Dania APPLICANT: Mood, William, I.

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: U2/09/902,759

CURRENT FILING DATE: 2001-07-10

FRIOR APPLICATION NUMBER: PCT/US00/0414

PRIOR FILING DATE: 1999-07-06

PRIOR APPLICANTION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICANTION NUMBER: US 60/146,222

PRIOR APPLICANTION NUMBER: DCT/US99/20594

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICANTION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-05

PRIOR PELING DATE: 1999-11-20

PRIOR PELING DATE: 1999-12-00-15

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR PELING DATE: 1999-12-00-15

                                                                                                                                                                                                                                   Sequence 200, Application US/09902759; Publication No. US20030077654A1; GENERAL INFORMATION: APPLICANT: Genentech, Inc.
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Goddard, A.
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APPLICANT: Pani, Vanne F.
APPLICANT: Pani, James
APPLICANT: Pani, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Scretted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Scretted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/665,350
PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-08
PRIOR PLILING DATE: 1999-07-08
PRIOR PLILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-18
PRIOR PLILING DATE: 1999-09-13
PRIOR PLILING DATE: 1999-09-13
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-00-05
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CTAGTGCTTGCTCTTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerriteen, Mary E.
Goddard, A.
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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US-09-902-634-200
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PFLING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 200
LENGTH: 2372
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APPLICANT: Pan, James
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APPLICANT: Pani, Nicholas F.
APPLICANT: Pani, Nicholas F.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, P. Mickey
APPLICANT: Wood, William, P. Mickey
APPLICANT: Wood, William, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION NUMBER: US/09/902,713
CURRENT APPLICATION NUMBER: US/0665,350
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
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PRIOR PILING DATE: 1999-07-28
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                                                                             GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
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           ; Sequence 200, Application US/09902713; Publication No. US20030082541A1; GENERAL INFORMATION:
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
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CORGANISM: Homo Sapien
US-09-902-634-200
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Query Match:
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                                                    ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLySLySLeuIle
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                           GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
                                                                                                                                             ceraciaeraerecreerecreerrecaerrecaerrerarrecaegaaaaaarrearr
                                                                                                                                                                                                                                                                      GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
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                                                                                                                                                                                       CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
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CURRENT APPLICATION NUMBER: US/09/907,979
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
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Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, A.
Goddwski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 200, Application US/09907979; Publication No. US20030082542A1; GENERAL INFORMATION:
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR PPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
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PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PRILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-16
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PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1090-12-20
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CORGANISM: Homo Sapien
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LENGTH: 237
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                                 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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                                                                           520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
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Publication No. US20030092002A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Filvaroff, Ellen
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Mather, Jennie P.
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Eaton, Dan L.
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US-09-902-615-200
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            PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-10-06
PRIOR PELING DATE: 1999-10-06
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1990-12-06
PRIOR PELING DATE: 1990-12-06
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FILING DATE: 2000-02-22
APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
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US-09-907-979-200
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ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                            LeuvalLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
                                                                                                                940 AGGIATGIGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
                                                                                                                                                          LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
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CURRENT APPLICATION NUMBER: US/09/903,925

CURRENT APPLICATION NUMBER: US/09/903,925

CURRENT APPLICATION NUMBER: US/09/903,925

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-02-2

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-18

PRIOR PRILOATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, James
Pan, James
Pan, James
Panni, Micholas F.
Roy, Margaret Ann
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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US-09-903-925-200
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/99/902,615
CURRENT APPLICATION NUMBER: US/99/902,615
CURRENT FILING DATE: 2001-12-14
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 200
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ORGANISM: Homo sapiens
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Best Local Similarity:
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1060 GATAAAAACCCAGAAGAGTCCAAGATCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT 1119
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                                                                                                                                                   GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
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      700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT 759
                                                                              940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATGGAAACC
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                                           CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
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APPLICANT: Walliam, P. mickey
TITLE OF INVENTION: Secreted and Transmembrar
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,760A
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
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Godowski, Paul J.
Grimaldi, Christopher J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleon
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Matches:
          FRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PELICATION NUMBER: PCT/US99/28313
PRIOR PELICATION NUMBER: PCT/US99/28313
PRIOR PELICATION NUMBER: PCT/US99/28564
PRIOR PELING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PELICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-05
PRIOR FILING DATE: 1999-12-05
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1060 GATAAAAACCCAGAAGAGTCCAAGGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT 1119
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              TGTGTCACAGAAGTTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTGTT
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                                                      GluPhelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
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CURRENT APPLICATION NUMBER: US/09/903,823
CURRENT FILING DATE: 2001-07-11
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Goddowski, Paul J.
Grimaldi, Christopher J.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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o. US20030104381A1
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Wood, William, I.
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Paoni, Nicholas F.
Roy, Margaret Ann
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
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                 460 AGCCCAAACCCCAAGTGTGGGAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG 519
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                                                                SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle
                                                                                                                520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Ellen
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Kljavin, Ivar J.
Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR FILING DATE: 1999-09-13
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; ORGANISM: Homo Sapien
US-09-903-823-200
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Botsein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napolec
APPLICANT: Filvaroff, Eller
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Woold, williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REPRESENCE: 10466-14
CURRENT FILING DATE: 1020-01-16
FRIOR FILING DATE: 1090-02-22
FRIOR FILING DATE: 1090-02-22
FRIOR FILING DATE: 1090-02-22
FRIOR FILING DATE: 1090-00-30
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FRIOR FILING DATE: 1090-03-16
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FRIOR PLICATION NUMBER: DCT/US99/2094
FRIOR FILING DATE: 1090-03-16
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FRIOR PLILING DATE: 1090-03-15
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; ORGANISM: Homo sapiens
US-09-907-652-200
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                                                  460 AGCCCAAACCCCCAAGTGTGGGAAAAATGGGGTGTGTGTCCTGATTTGGAAGGTTCCAGTG
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; Publication No. US20030113718A1
; GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napolec
APPLICANT: Firstar, Napolec
APPLICANT: Firstar, Napolec
APPLICANT: Gao, Wei-Qang
APPLICANT: Gao, Wei-Qang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Mary
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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
FILE REFERENCE: 10466-14
FILE REPERENCE: 10466-14
FILE REPERENCE: 10466-14
FILE REPERENCE: 10466-14
FRIOR APPLICATION NUMBER: US 60/145,698
FRIOR PILING DATE: 1999-07-26
FRIOR PELING DATE: 1999-07-26
FRIOR PELING DATE: 1999-07-28
FRIOR FILING DATE: 1999-09-13
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NUMBER OF SEQ ID NOS: 423
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Hillan, Kenneth, J
Kljavin, Ivar J.
Mather, Jennie P.
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Roy, Margaret Ann
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SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle
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                                                     340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAAACAGCTTGAAAGCT
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                          CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
                                                                                                                                                   400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT
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| Publication No. US20030113719A1
| Publication No. US20030113719A1
| APPLICANT: Genentech, Inc. | APPLICANT: Ashkenazi, Avi | APPLICANT: Betsein, David | APPLICANT: Betsein, David | APPLICANT: Eaton, Dan L. | APPLICANT: Fairara, Napoleone | APPLICANT: Filvaroff, Ellen | APPLICANT: Fong, Sherman | APPLICANT: Gerber, Hanspeter | APPLICANT: Gerber, Hanspeter | APPLICANT: Gerritsen, Mary E.
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                        APPLICANY: Stewart, Innochy Applicany: Stewart, Innochy Applicany: Stewart, Innochy Applicany: Stewart, Innochy Applicany: Williams, Daniel
APPLICANY: Williams, Daniel
APPLICANY: Williams, Daniel
ITITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/902,979
CURRENT APPLICATION NUMBER: US/09/902,979
CURRENT APPLICATION NUMBER: US/09/665,350
PRIOR PELING DATE: 1090-07-10
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Stewart, Timothy A.
Tumas, Daniel
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RRIOR REPLICATION NUMBER: PCT/US99/30099
RRIOR APPLICATION NUMBER: PCT/US99/30099
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RRIOR REPLICATION NUMBER: PCT/US99/30099
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Godowski, Paul J.
Grimaldi, Christopher
                                 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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                                                                                                          220 GTCCAAGGCTCTTTGCGTGCAGAAGCTTTTCCATCCAGGTGTCATGCAGAATTATGGGG
                                                                                                                                                                                                                                                                     460 AGCCCAAACCCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
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                                                                 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArglleMetGly
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US-09-906-815A-200
Sequence 200, Application US/09906815A
Publication No. US20030113838A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
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160 639

669 200 759 819 240 879

300

321 GluVal 322

2372 322

Length: Matches:

322.00

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SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal 120
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                                                                                                                                                          MetAlaArgCysPheSerLeuValleuLeuLeuThrSerIleTrpThrThrArgLeuLeu
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Mismatches:
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          Percent Similarity:
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### PELICANT: Wood, Williams, P. Mickey
### PELICANT: Wood, Williams, P. Mickey
### PELICANT: Wood, Williams, P. Mickey
### PELICANT: Wood, Williams, P. Mickey
### PELICANTON NUMBER: US/09/906, #ISA
### CURRENT FILING DATE: 2010-07-16
### PRIOR APPLICATION NUMBER: US/09/0414
### PRIOR APPLICATION NUMBER: US/09/0414
### PRIOR APPLICATION NUMBER: US/09/0414
### PRIOR PLING DATE: 1099-07-26
### PRIOR PLING DATE: 1999-07-26
### PRIOR PLING DATE: 1999-07-26
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                                                                                                                                                               Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                               Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                        Gurney, Austin L.
Hillan, Kenneth, J.
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; ORGANISM: Homo
US-09-906-815A-200
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Score:
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Search completed: September 16, 2004, 05:29:16 Job time : 2347 seca

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on:   September 15, 2004, 03.45:39; Search time   September 15, 2004, 03.45:39; Search time   September 15, 2004, 03.45:39; Search time   Sequence: 2029   1134.446 Million cell updates/sec   2029   2020   2		nuciero segion, using sw moder	
US-10-079-111-2  10-079-111-2  11-0-079-111-2  12-029  13-0272 seq9, 21671516995 residues  13-0274:  13-0274: 1	: uo	<pre>15, 2004, 03:45:39 ; Search time 7898 Se (without alignments) 11134.846 Million cell</pre>	
table: IDENTITY NUC  Gapop 10.0 , Gapext 1.0  Bayo 10.0 , Gapext 1.0  DB seq length: 200000000  Coessing: Minimum Match O%  Maximum Match O%  Listing first 45 summaries  GenEmbl:*  1: 9b ba:*  2: 9b ba:*  3: 9b ln:*  4: 9b ln:*  5: 9b ln:*  6: 9b ln:*  7: 9b ln:*  10: 9b ln:*	score: 20:::	2 agaagcttaaacatttaaaaaaaaa 202	
d: 3470272 seqs, 21671516995 residues  umber of hits satisfying chosen parameters:  DB seq length: 200000000  Occessing: Minimum Match 100%  Listing first 45 summaries  Asximum Match 100%  Listing first 45 summaries  GenEmbl:*  1: 9D ba:*  3: 9D ha:*  4: 9D ph:*  5: 9D ph:*  8: 9D ph:*  10: 9D pr:*  11: 9D ph:*  12: 9D ph:*  13: 9D ov:*  5: 9D ph:*  14: 9D vi:*  15: 9D ph:*  16: em fun:*  17: em ov:*  18: em ov:*  22: em ov:*  23: em ph:*  24: em ph:*  25: em ph:*  25: em ph:*  26: em fun:*  27: em fun:*  28: em htg-inv:*  29: em htg-inv:*  39: em htg-inv:*  30: em htg-inv:*  40: e	table:	TTY_NUC 10.0 , Gapext	
umber of hits satisfying chosen parameters:  DB seq length: 0  DB seq length: 200000000  Ocessing: Minimum Match 100*  Listing first 45 summaries  GenEmbl:*  1: gb ba:*  2: gb htg:*  3: gb ow:*  6: gb pat:*  7: gb pat:*  10: gb pat:*  11: gb ba:*  12: gb htg:*  13: gb ow:*  14: gb ow:*  15: gb pat:*  16: gb pat:*  17: mm hum:*  18: mm ba:*  19: mm ba:*  11: gb ste:*  11: gb ste:*  12: gb w:*  13: gb un:*  14: gb w:*  15: mm ba:*  16: mm ba:*  17: mm hum:*  18: mm ba:*  19: mm ow::*  20: mm ow::*  21: mm ow::*  22: mm pat:*  23: mm pat:*  24: mm ph:*  25: mm htg other:*  26: mm htg other:*  27: mm ftg mus:*  28: mm htg other:*  39: mm htg other:*  31: mm htg other:*  32: mm htg other:*  33: mm htg other:*  34: mm htg other:*  35: mm htg other:*  36: mm htg other:*  37: mm htg other:*  38: mm htg other:*  39: mm htg other:*  30: mm htg		seqs, 21671516995	
DB seq length: 0  DB seq length: 200000000  In string first 45  Elsting first 45  El	number of	satisfying chosen parameters:	
e: Gensming: Minimum Match 0%  Maximum Match 100  Listing first 45  Gensmbl:*  1: 9D ba:*  2: 9D ba:*  3: 9D in:*  4: 9D ov:*  6: 9D pat:*  7: 9D pat:*  10: 9D ro:*  11: 9D ro:*  12: 9D vi:*  13: 9D ui:*  14: 9D vi:*  15: em ba:*  16: em fun:*  17: em hum:*  18: em pi:*  22: em ov:*  22: em ov:*  23: em pt:*  24: em pi:*  25: em pt:*  26: em pt:*  27: em sts:*  28: em htg.nn:*  30: em htg.nn:*  31: em htg.nn:*  33: em htg.nn:*  34: em htg.nn:*  35: em htg.nn:*  36: em htg.nn:*  37: em htg.nn:*  38: em htg.nn:*  38: em htg.nn:*  38: em htg.nn:*  39: em htg.nu:*  30: em htg.nu:*  40: em htg.nu:*	DB seq DB seq		
e: GenEmbl:*  1: 90 ba:*  2: 90 htg:*  4: 90 om:*  4: 90 ow:*  5: 90 ov:*  6: 90 ov:*  7: 90 pa:*  10: 90 pa:*  11: 90 pa:*  11: 90 pa:*  11: 90 vi:*  13: 90 ui:*  14: 90 vi:*  15: em_ba:*  16: em_fun:*  17: em_lum:*  18: em_lum:*  19: em_lum:*  20: em_or:*  21: em_lum:*  22: em_lum:*  22: em_lum:*  23: em_ltg_lum:*  24: em_ltg_lum:*  25: em_ltg_lum:*  26: em_ltg_lum:*  27: em_ltg_lum:*  28: em_ltg_lum:*  39: em_ltg_lum:*  31: em_ltg_lum:*  34: em_ltg_lum:*  34: em_ltg_lum:*  35: em_ltg_lum:*  36: em_ltg_lum:*  37: em_ltg_lum:*  38: em_ltg_lum:*  39: em_ltg_lum:*		Match 0% Match 100 first 45	
100		**************************************	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Description			BD222/18 AR410761	AX092274	AX45446	AX490924	AX697609	BD075532	117337 11737111	BD173030		BD175383	AY358925		AX136227		AK075443 Homo		AY372937 Bos t	AX136529 Seque	BD123769 Secre		1 AJ311501 Mus	AX331191 Seque	AX331600	AX332298 AX3333350	AX333777	AX407467	AX136672 Seque	BD123912 R1076146	AY304537 Sus s	BD073800 5'EST	BD077623 5'EST	5239 AXIS6239 Sequence 3816 Sequence 3816	AR283312 Sequenc	AR344080 Sequenc	AR351281 Sequenc	AX303004 S	ALIGNMENTS		129 bo DNA linear PAT 20-JUN-2002					one of other		
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361 CCTGTAGGCTGCGGCTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAG 420	ANTIATCACCACAAGATCCCATATTCAACACTCAAACTGCAACCAAACAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACCAAACAATTATCACCACCAAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAATACCTATTCAGTGAAATTATTATTCAGTGCATCCCTTACTCTACTACTACAAAATTATTATTATTCAGTGCATCCCCTTACTCTACAAAAATTATTATTATTATTATTAT		
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Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                              Patent: WO 0116318-A 5 08-MAR-2001;
Genentech, Inc. (US)
Location/Qualifiers
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Best Local Similarity 99.8%;
Matches 1997; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            TCAGGACTGCCATTGGACTATGGAGTGCCACCAAAGAGAATGCCCTTCTCTTATTGTAAC
                                                                                                               GTCCTAATAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGACCTAAAACATC
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Qy 1944 GAGTTACAGAATTACTACGAAGATTACTCAGAAATTACTTAC		RESULT 5 AX454446 LOCUS AX454446 2372 bp DNA linear DEFINITION Sequence 31 from Patent W00208284.	AX45446 AX45446.1 GI:21713847 Homo caniens (himan)	ORGANISM Homo Saptens Annuan, ORGANISM Homo Saptens Eukaryota; Metazoa; Chordata; Craniata; Vertebrat; Mammalia; Eutheria; Primates; Catarrhini; Hominid	AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams	TITLE Compositions and methods for the diagnosis and tradisorders involving angiogenesis JOURNAL Patent: WO 02008284-A 31 31-JAN-2002; Genentech Inc (18): Raker. Kevin P. (US): Fex.	(US); Gerber, Hanspeter (US); Gerritsen, Mary E Audrey (US); Godowski, Paul J. (US); Gurney, Au Hilan, Kenneth J. (US); Marsters, Scot A. (US); Danish Mary E (US)	Watanabe, Colin K. (US); Williams, P. Mickey (US) I. (US) Location/Qualifiers	5	Query Match 98.3%; Score 1994; DB 6; Length Best Local Similarity 99.8%; Pred. No. 0; Marches 1947. Conservative 0: Mismatches 5: Indels	ACCGGATGTCTCGGTTATGAAGTGGAGCAGT		144	204	264 2	324	384
4 AATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGCT	924 TTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT 983 91 TTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT 960	984 TITACAAACAAGAATCAGCAGAAAGGAAATGATCGAAAGCAAAGTAGTAAAGAGAGAAGA 1043 	1044 GCCAATGATAGCAACCTAATGAGGAATCAAAGAAAACTGATAAAAACCCAGAAGAGTCC 1103 	1104 AAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1163 	1164 TGAGGAGACACCTGAGGCTGGTTCTTTCATGCTCCTTACCCTGCCCCAGCTGGGAA 1223 	1224 ATGAAAAGGCCGAAAGAACGAAAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC 1283 	1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGCCCTTCTCCTTATTGTAAC 1343 	1344 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCCAGGCCTTTCTAGCCTGCTAT 1403	1404 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGACCTAAAACATC 1463 	1464 TCATCAGTATCCAGTGGTAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGAGTTGAAAGC 1523 	1524 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA 1583 	1584 GCTCTGAAAGAGAAACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1643 	1644 AGAATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1703 	1704 TCTCTGTABAGCTABABABABABABABABABABAGGCTGAGGATACGACAGTACACTGTCA 1763 	1764 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT 1823 	1824 CACTGTTTAGAACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1883 	1884 AGGAAATATACTTTTACAAGTAACAAAAAACTCTTATAAATTTCTATTATCT 1943 
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, E. (US); Goddard,
Austin L. (US);
S); Pan, James (US)
ippe F. (US);
(US); Wood, William Ir PAT 06-JUL-2002 o O CATATCACCAGTGGC 143 AGGTGCTTCAGCCTG 203 ata; Euteleostomi; (dae; Homo. Goddard, A.,
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444 GGCTGGGTTGGAGATTCGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGGG 503 421 GGCTGGGTTGGAGATTCGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGGG 480 504 AAAATGGGGTGGGTTCGATTTGGAAGGTTCCAGGATTTGCAGCCTAT 563 481 AAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACGTTTGCAGCCTAT 540 564 TGTTACAACTCATCTGATTTGGAAGGTTCCAGTGAGCCGACGTTTGCAGCCTAT 540 565 TGTTACAACTCATCTGATACTTGGAAGGTTCCAGGAAATTATCACCACCAAA 600 624 GATCCCATATTCAACACTCGACTAACTCGTGCATTCCAGAAATTATCACCACCAAA 600 625 GATCCCATATTCAACACTCGAACACACAAACAAATTATTGTCAGTGACCAA 600 626 GATCCCATATTCAACACTCAAACTCGTGCATTCCAGAAATTATTGTCAGTGACAGT 660 686 GATCCCATATTCAACACTCAAACTCGTGCATTCCAGAAATTATTGTCAGTGACAGT 600 697 GATCCCATATTCAACACTCAAACTCGTGCATTCAGTACTCGTCCTCCTGT 73 661 GATCCCATATTCAACACTCAAACTCGTCAAACAAATTATTGTCAGTGACAGT 600 686 AACTACTCGGTGGCATCCCAAACAAAAAATTGATTTATTGTCAGTGACAGT 720 744 CCAGCTTCCACTTCTATTCCACAAAAAAAATTGATTTGTCACAGAAGTTTTTATG 803 721 CCAGCTTCCACTTCTATTCCACGAAAAAAAATTGATTTGTCACAGAAGTTTTTATG 780 721 CCAGCTTCCACTTCTATTCCACGAAAAAAAAATTGATTGTCACACAAGATTTTATG 780 721 CCAGCTTCCACTTCTATTCCACGAAAAAAAAAAAAAAAA	984 TITACAACAAGAATCAGCAGAAGGAATGATCGAAACCAAGGTAAAGGAGGAGAGA 1023

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CILNIS,09,C07K14/47,C07K14/705,C07K16/18,C07K16/28,C07K19/00,
C12N1/19,
C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02//(C12P21/08, PC
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Location/Qualifiers /organism="Homo sapiens" /organism="Homo sapiens" /mol_type="genomic DNA"
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059113,14-SEP-1997 US
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059113,14-SEP-1997 US
062287,17-OCT-1997 US
063348,24-OCT-1997 US
063120,24-OCT-1997 US
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60/06287,17-0CT-1997 US
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60/063120,29-0CT-1997 US
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OS Homo sapiens (human)
PN UP 201516580-A/165
PD 02-OCT-2001
PF 16-SEP-1998 UP 2000511867
PR 17-SEP-1997 US 60/059115
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JP 2001516580-A/165.
Homo sapiens (human)
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PAT 18-FEB-2003 acids encoding

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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JIAN ZHENG,
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Patent: JP 2002223786-A 165 13-AUG-2002;
GENENTECH INC
OS Homo sapiens (human)
PN JP 200223786-A/165
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PF 18-DEC-2001 JP 2001385135
PR 17-SEP-1997 US 60/059115,17-SEP-15
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Homo sapiens (human)
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                                                                                                                 Patent: JP 2002238886-A 165 27-AUG-2002; GENENTECH INC
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/ organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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QY         1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGCCCTTCTCCTTATTGTAAC 1343           Db         1261 TCAGGACTGCCATTGGAGTGCACCAAAGAGAATGCCCTTCTCCTTATTGTAAC 1320           QY         1344 CCTGTCTGCATCTTCTCTCCTCCAAAGATTCCCACGGCCTTTCTAGCCTGGCTAT 1403           Db         1321 CCTGTCTGGATCCTACCTCCTCACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTAT 1380           QY         1404 GTCCTAATAATATCCCACTGGAGAAAGAGTTTTGCAAAGTGCAAGGACCTAAAACAT 140           Db         1381 GTCCTAATAATATCCCACTGGGAGAAAGAGTTTTGCAAAGTGCAAGGACCTAAAACAT 140           QY         1464 TCATCAGTATCCAGTGGTAAAAAGAGCCTCCTGGCTGTGTGAAGGTGCAAGGACCTAAAAACAT 1500           QY         1524 CAAGGAGTAACCAAGGATAACAAGAGTTCTCTACTGAGGCTAAGAGCTTCTACAAGC 1500           QY         1524 CAAGGAGTCACTGAGACCAAGGCTTCCTCTACTGAGGCTCAGACCTTTCTTCA 1583           Db         1501 CAAGGATCACTGAGACCAAGGCTTTCTTCTCTACTGAGTCTCAGACCTTTCTTCA 1583           Db         1501 CAAGGAGTCACTGAGACCAAGGCTTTCTTCTCTACTGAGTCCGCAGCTCAGACCTTTCTTCA 1560           QY         1584 GTCTGAAAAAAAGACCAAGGCTTTCTCTCTACTGATTCCGCAGCTCAGACCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTC	Db   1561   GCTCTGAAAGAGAAACACGTTCCCACCTGCTTCTGTGCCCGGTAAGAGCAAA   1620	Db   1741	Qy         2004 TTCAACAAACATTTAAAAAAAA 2025           Db         1981 TTCAACAACATTTGCTGAATA 2002           RESULT 11	the same. BD17303.0 BD17303.0 BD17303.0 BD17303.0.1 GI:28414336 JP 2002238587-A/165. JP 2002238587-A/165. Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 2372) Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. a Yuan, J. Secreted and transmembrane polypeptides and nucleic acids the same Patent: JP 2002238587-A 165 27-AUG-2002; GENENTECH INC

\$63 AAAAATGGGGTGGGTGCCTGATTTGGAAGGTTCCAGTGAGCCGACACATTGCAGCCTAT 563  481 AAAATGGGGTGGGTGCCTGATTTGGAAGGTTCCAGTGAGCCGACACTTTGCAGCCTAT 540  481 AAAATGGGGTGGGTGCCTGATTTGGAAGGTTCCAGTGAGCCGACACTTTGCAGCCTAT 540  564 TGTTACACTCTCTCTCTGATACTTGGACTTACTCCAGAAATTATTGCACCACCAA 623  51 TGTTACAACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATTATTGCACCACCAA 600  624 GATCCCATATTCAACACTCAAACTGCAACAACAACAACAAATTATTGTCAGTGACAGT 660  684 ACCTACTCGGTGGCATCCCCTTACTCTACAACAACAACAACAAATTATTGTCAGTGACAGT 660  684 ACCTACTCGGTGGCATCCCCTTACTCTACAAACAACAACAACTACTACTCCTC	01 TTTGGTGCTGCAGCTCGTCGGATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCT 84 TTTACAAACAAGAATCAGCAAAGGAATGATCGAAACCAAAGTATGTGAAGGCCTTCCCT 85 TTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGGAGAGGAGAAGTTTACAAACAA	1044   GCCAATGAIAGCAACCCTAATGAGGAATCAAAGAAACTGATAAAAACCCAGAAGGTCC   1103	1164 TGAGGAGACACACCTGAGGTTTCTTTCATGCTCCTTACCCTGCCCGGCTGGGGGAA 1223	1284   TCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGCCCTTCTCCTTATTGTAAC 1343	1404 GTCCTAATAATATCCCACTGGGAAAAGAGTTTTGCAAAGTGCAAGGACCTAAAACTC 1463  1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGACCTAAAACATC 1440  1464 TCATCAGTATCCAGTGGTAAAAAGGCTTCTGGCTGTTGAGGTGGTGGGTTGAAAGC 1523  1441 TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTTGTGGTGGTTGAAAGC 1500  1524 CAAGGGTCATGAGACCAAGGCTTTCTACTGATTCCGCAGCTCAGGTTGAAAGC 1500  1524 CAAGGAGTCATGAGACCAAGGCTTTCTTCTACTGATTCCGCAGCTCAGACCTTTCTTCA 1583  1501 CAAGGAGTCATGGAACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA 1560  1584 GCTCTGAAAGAGAACACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA 1560
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	FEATURES fl Location/Qualifiers (human)'.  Source 12372 /organism="Homo sapiens" /mol type="genomic DNA" /db_xref="taxon:9606"	Query Match         98.3%;         Score 1994;         DB 6;         Length 2372;           Best Local Similarity         99.8%;         Pred. No. 0;         No. 0;           Matches 1997;         Conservative         0;         Mismatches         5;         Indels         0;           Qy         24 AGCAGGGAAATCCGGTTATGAAGTGGAGCAGTGAGGCCTCAACATA         83           Db         1 AGCAGGAAATCCCGATGTCTCGGTTATGAAGTGGAGCAGTGAGTG	QY         84 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCGGTGGC 143           Db         61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120           QY         144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGGTGCTTCAGCTG 203           Db         121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCATGGCTTCAGCTG	STGCA STGCA STGCA AAAAG	AAGT

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A61P25/00,
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60/066346,118-NOV-1997 US 60/065186 PR
60/066120,21-NOV-1997 US 60/065693 PR
60/066772,24-NOV-1997 US 60/066364 PR
60/066772,24-NOV-1997 US 60/066466 PR
60/066773,24-NOV-1997 US 60/066416 PR
60/06673,25-NOV-1997 US 60/066410 PR
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J.,
Yuan, J.
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GENENTECH INC

OS Homo sapiens (human)

PD 10-28P-2002

PP 10-28P-2001

PP 18-DEC-2001 JP 2001385319

PR 17-SEP-1997 US 60/059115,17-SEP-
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                     CCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGA
                                                                 TGGATTCGTGGTCATCTCTAGGATTAGCCCCAAACCCCCAAGTGTGGGGAAAAATGGGGTGGG
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247. .480
/note="Region: Link domain"
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Jackson, D.G., Banerji, S. and Ni, J.
Direct Submission
Submitted (06-JAN-1999) MRC Human Immunology Unit, Univ. of Oxford, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK
                                                                                                                                                                                                                                       Jones, M.
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1 (Joases I to 2313)

Banerii,S., Ni,J., Wang,S.X., Clasper,S., Su,J., Tammi,R., Jones,M. and Jackson,D.G.

LYVB-1, a new homologue of the CD44 glycoprotein, is a lymph-specific receptor for hyaluronan

J. Cell Biol. 144 (4), 789-801 (1999)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

REFERENCE AUTHORS TITLE JOURNAL COMMENT

Homo Saplens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1143)

S.S. Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:12934166.

Contact: Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 seqrefagenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSODI039DE03NP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :

AL574194 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA Clone CSODI039XJ06 3-PRIME, mRNA sequence.
AL574194
AL574194.2 GI:31295529
EST.

RESULT 1 AL574194/c LOCUS DEFINITION Homo sapiens (human) Homo sapiens

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

ALIGNMENTS

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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
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Pred, No. 1.6e-202;
8; Mismatches 20; Indels
http://fulllength.invitrogen.com/
Faraday Avenue Genoscope sequence
Location/Qualifiers
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1668 1728 1729 TAGAACAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAACACAGAGAGG 1788 EST 31-MAY-2003 186 126 AL550279
AL550279 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA. 99 CICTCATATCACCAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGAT 184 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: sequefégenoscope.ons.fr, www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see /mol type="miner" supremental control of the property of the p 305 KCCIGACATGTCCTTCTGAGCCCGGTAAGAGCAAAAGAGGGGGDARRGTTJAGCCCCK GAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAAATAAAGAAA GAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAAAGCTAAAATAAAGAAA ACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAAAGAATGGCAGAAAAGTTTAGCCCCT Contact 185 TAGAACAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAACACAGGGG http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1039DE03QP1&cluster=5952.r. Contac cgi-bin/cluster.cgi?seq=CS0D1039DE03QP1&cluster=5952.r. Contac Feng Lidang Email : fliamg@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0D1039DE03QP1. gi:12887098 Length 1154; 2; On Feb 15, 2001 this sequence version replaced Contact: Genoscope 1 (bases 1 to 1154)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Unpublished (2001) Score 1043.8; DB 9; Pred. No. 1.4e-200; 1; Mismatches 6; I 1849 ITTICIGGICTCTACCACTGCTGATATTTTCT 1881 33 /organism="Homo sapiens"

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Li (Bases I to 1201)
Li, W.B.; Gruber, C.; Jessee, J.; and Polayes, D.
Full-length cDNA libraries and normalization
Ombublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12887768.
Contact: Genoscope
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-Oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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cgi.bin/cluster.cgi?seq=CSODIOSBDG070Pl&cluster=5952.r. Contact
cgi.bin/cluster.cgi?seq=CSODIOSBDG070Pl&cluster=5952.r. Contact
Feng Liang Email : fliang@lifeten.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIOSBDG07QPl.
Location/Qualifiers
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r
more information about this cluster, see
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AL550621 Homo sapiens PLACENTA COT 25-NORMI
clone CSODIO58YN14 5-PRIME, mRNA sequence.
AL550621.2 GI:31272438
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BP 191 91006 EVRY cedex - France
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/db_xref="taxon:9606"
/clone="CS0D1058YN14"
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  CTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGAT
                                                                                      GGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGT
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/mol_type="mRNA"

db_xref="taxon:9606"
/clone="cSODI0674018"
/tissue type="HPLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BCOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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94.7%; Pred. No. 1.4e-182;
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AL552625 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI067YG15 3-PRIME, mRNA sequence.
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Contact: Genoscope
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BP 191 91006 EVRY cedax - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=cSODIO67AD08NP1&cluster=5952.r. Contact :
Feng Liang Email: fliang@lifetech.com URL: Contact :
Feng Liang Email: fliang@lifetech.com URL: Contact :
Faraday Avenue Genoscope sequence ID : CSODIO67AD08NP1.
                       GGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCCGACAGCTATTGTTAC
                                                                                                                                                                                                                                               TCGGTGGCATCCCCTTACTCTACAATACCTGCCCCTACTACTACTCCTCCTGCTCCAGCT
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                                                                                                                                              ATATTCAACACTCAAACTGCAACACAACAACAACAGAATTTATTGTCAGTGACAGTACCTAC
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                                                                                                         AACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCC
                                                                                                                                                                                                                      TCGGTGGCATCCCCTTACTCTACAATACCTGCCCCTACTACTACTCCTCCTGCTCCAGCT
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                                                                                                                  GCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGG
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COT 25-NORMALIZED Homo sapiens CDNA
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BcoR V
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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ACCTAATCTCTGTAAAACTAAAATAAAAATAGAACAAGGCTGAGGATACGACAGTACA
                                                                                                                TGGAATCACTGTTTAGAACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: sequefegenoscope.ons.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r F
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI029AGI2NPl&cluster=5952.r. Contac
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI029AGI2NPl.
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Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12879852
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                                                                                                                                                                                                                                                                                                                            AL546590 nRNA 1201 bp mRNA AL546590 Homo sapiens PLACENTA COT 25-NORM Colone CSOD1029YM23 3-PRIME, mRNA sequence. AL546590
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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/db_xref="taxon:9606"
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E. (Dasses 1 to 1157)

Full-length cDNA libraries and normalization

In pubblished (2001)

On Feb 16, 2001 this sequence version replaced gi:12936752.

Contact: Ganoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Genoscope - Centre National de Sequence cluster 5952.

Email: seqrefégenoscope.cns.fr whe: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODIO59BA06NDI&cluster=5952.r. Contact :
Feng Liang Email: fliangelifetech.com URL:

Feng Liang Email: fliangelifetech.com URL:

Franday Avenue Genoscope sequence ID : CSODIO59BA06NPI.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
CCCTTACTCTACAATACCCTGCCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTAT
                                                                                                                                                                                                 TCCACGGAGAAAAAATTGTTTTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTC
                                                                                                                                                                                                                                                        TACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTT
                                                                                                                                                                                                                                                                                            TACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTT
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                                                                                                                                                                TCCACGGAGAAAAATTGATTTGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTC
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AL575514 Homo sapiens PLACENTA COT 25-NORWALIZED Homo
AL575514 Homo SAPALZ 3-PRIME, mRNA sequence.
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Pred. No. 3.6e-179;
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/clone="CS0DI059YA12"
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              E 1 (bases 1 to 1015)

S Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12891068.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.gi?seq=CSD01069DG01QP1&cluster=5952.r. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1069DG01QP1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.2e-180;
0; Mismatches 2;
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                                        AUTHORS
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	more into about this cluster, see http://www.genoscope.cns.fr cgi-bin/cluster.cgi?seq=CSOA1040CB02QPl&cluster=5952.r. Contact:	ORIGIN  Query Match  46.1%; Score 936; DB 13; Length 1201;  Best Local Similarity 97.6%; Pred. No. 8.2e-179;  Matches 953; Conservative 15; Mismatches 6; Indels 2; Gaps 2;  Qy  46.364; Pred. No. 8.2e-179;  Atches 953; Conservative 15; Mismatches 6; Indels 2; Gaps 2;  Qy  47.464; Pred. No. 8.2e-179;  Qy  48.184; Pred. No. 9.2e-179;  Qy  48.184; Pred. No. 9.2e-179;  Qy  48.184; Pred. No. 9.2e-179;  Qy  48.184; Pred. No. 95 CTCCATCCGGATGAGGAGGAGTGAGGTGAGGAGGAGGTGAGGAGGTGAGGAG	155 TTTCCCTGGCTCTGAGGGGTAGGCCAGGTGCTTCGGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGT
Matches 960; Conservative 23; Mismatches 23; Indels 3; Gaps 2;           Qy 915 CTCCTCTTCTTGGTGCTGCAGCTGGTCTTGGATTTGCTATGTCAAAGGTATGTGAAG 974	1215 GCTGGGGAAATCAAAGGCCAAAGAACCAAAGAAAAGTCCACCCTTGCTTCCTAACT  1215 GCTGGGGAAATCAAAGGGCCAAGAACCAAAGAAGAACCCACCC	DD 529 CCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGGACC 470  QY 1455 TAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCTCTCTGGGTTTTGCAAGGTGG 1514  DD 469 TAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCTCTCTGGGTTCTGAGGTGG 110  QY 1515 GTTGAAAGCCAAGAGTCACTGAGACCAAGGCTTCTCTCATTCGCAGTCGAGTGG 410  DD 409 GTTGAAAGCCAAGAGTCACTGAGACCAAGGCTTCTTCTATTCGCAGCTCAGACC 350  QY 1575 CTTTCTTCAGCTCTGAAAGAAAAAGTTTAGCCCACCTGACATCCTTCTGAGCCGGT 1634  DD 349 CTTTCTTCAGCTCTGAAAGAAAAAGTTTAGCCCACCTGACATCCTTCTGAGCCCGGT 290  OV 1635 AAGAGCAAAAGAAAAAGTTTAGCCCCTGAAAAGCTTCTCATAACTT 1694	289 AAGAGCAAAAGAATGCCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTT 1695 GAGACCTAATCTCTGTAAAGTTATAGCCCCTGAAAGCCATGGAGATTCTCATAACTT 229 GAGACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGT 1755 ACATGTCAGCAGGGACTGTAAACACAGACAGACAAAGCTAAAGCTAAAGCAAAAGCTAAAAGCTAAAAGAAAAAGAAAG

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/db_xref="taxon:9606"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens Primed with a NotI-oligo(dT)
/clone="Ist strand cDNA was primed with NotI and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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E 1 (bases 1 to 1007)

E 1, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

To Feb 16, 2001 this sequence version replaced gi:12936986.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqrefégenoscope cns.fr. Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5952.r For

more information about this cluster, see
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AL575633.2 GI:31313940
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cgi-bin/cluster.cgi?seq=CSODI069DG01NP1&cluster=5952.r. Contac
gi-bin/cluster.cgi?seq=CSODI069DG01NP1&cluster=5952.r. Contac
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI069DG01NP1.
Location/Qualifiers
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1811 ATTGAGTTGGAATCACTGTTTAGAACACACACTTACTTTTTCTGGTCTCTA-CCACTG 1869		ORGANISM Homo sapiens  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  REFERENCE 1 (bases 1 to 1201)  AUTHORS Li, W. B., Gruber, C., Jessee, J. and Polayes, D.  TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished (2001)  COMMENT On Feb 15, 2001 this sequence version replaced gi:12882152.  Contact: Genoscope - Centre National de Sequencage  Genoscope - Centre National de Sequencage  BP 191 91006 EVRY cedex - France	Email: seqref@genoscope.ons.fr, Web: www.genoscope.ons.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see http://www.genoscope.ons.fr/ cgi-bin/cluster.cgi?seq=CSODI033CB06QP1&cluster=5952.r. Contact : Feng Liang Email : fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODI033CB06QP1. Location/Qualifiers Location/Qualifiers source /organism="Homo sapiens" /db_xref="Homo sapiens" /clone="CSODI033YP1" /clone="CSODI033YP1" /clone="CSODI033YP1" /clone="CSODI033YP1" /clone="CSODI033YP1" /clone="CSODI033YP1" /clone="CSODI033YP1"	/ Orde="1st straid cDNA was primed with a Not1-oilgo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized."  Query Match 46.0%; Score 932.8; DB 9; Length 1201;  Best Local Similarity 92.0%; Pred. No. 3.6e-178;  Matches 1003; Conservative 20; Mismatches 63; Indels 4; Gaps 4;  Qy 1 CCTTGACAAGTCAGAAGCTGAGAAATCCGGATGTTGTAGTAGTAGAGGGG 60	61 CAGTGAGTGTGAGCTCAACATAGTTCCAGAACTCTCCGTCCG

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AL552127
AL552127 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODIO59YAL2 5-PRIME, mRNA sequence.
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1 (Dases 1 to 1172)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Fill-length cDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12890728.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
           GCAACACAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTAC
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cgi-bin/cluster.cgi?seq=CSODI059BA06QPl&cluster=5952.r. Contac
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Feng Liang Email: fliangelifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI059BA06QPl.
Location/Qualifiers
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/mol_type="mRNA"
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/clone="CSODI059YA12"
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E 1 (bases 1 to 1201)

Liw, Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12880008.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr
cgi-bin/cluster.gi?seq=CSDD1029CED5QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://tulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI029CED5GP1.
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AARGTATTTTAAGGCTTCCYTTTAYAACAAATARCAGARGRAATGATCAAAMCAAATA 1076
                                                                       1022 CAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAAC 1081
                                                                                              AAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAAC 1021
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AL552661 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA Clone CSODI067YG15 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Umpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12891779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 TGCCTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCAC 181
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Genoscope - Centre National de Sequencage
BP 191 91006 EYRY cedex - France
Bmail: seqrefégenoscope.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1067AD08QPl&cluster=5952.r. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenu Genoscope sequence ID: CS0D1067AD08QPl.
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Pred. No. 2.3e-174;
5; Mismatches 10;
                                                                                                                                           TGATAAAACCCAGAAGAGTCCAAGAG 1108
                                                                                                                                                                         1137 ARRICMRVAAATACGKGGDKCKGRRVK 1163
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI067YG15"
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AL552661.2 GI:31274476
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                                                                                                                                                                                                                                                                                                                                                                        /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                 Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODIO58CEIONPI&cluster=5952.r. Contact
Feng Liang Email : fliang@alifetcech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope_sequence ID : CSODIO58CEIONPI.
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Pred. No. 4.6e-173;
1; Mismatches 10;
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                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI058YJ19"
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AL574433 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA Clone CS0DI058VJ19 3-PRIME, mRNA sequence.
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AL574433.2 GI;31312751
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Catarrhini, Hominidae, Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Lingth cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12934635.
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Mammalia; Eutheria; Primates;
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E. 1 (bases 1 to 1201)

I.i.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization

On Dreb 15, 2001 this sequence version replaced gi:12879917.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.ons.fr, Web: www.genoscope.ons.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0Dlo29Agi2cpl&cluster=5952.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0Dl029AGI2QPI.
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AL546623 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone CS0D1029YM23 5-PRIME, mRNA sequence.
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-Oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                  CTTGAGACCTAATCTCTGTAAAGCTAAAATAAAGAATAGAACAAGGCTGAGGATACGAC
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                                                                 AGTACACTGTCAGCAGGACTGTAAACACAGACAGGGTCAAAGTG
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI029YM23"
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DEFINITION
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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030124543A1 3044710CB1
US-10-079-111-2
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US-09-906-646-200

US-09-906-700-200

US-09-903-786-200

US-09-903-786-200

US-09-903-786-200

US-09-904-119-200

US-09-904-119-200

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US-09-907-615-200
US-09-903-925-200
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Publication No. US20300124543A1
GENERAL INFORMATION:
APPLICANT: Stratt, Susan G.
TITLE OF INVENTION: BREAST CANCER MARKER;
FILE REFERENCE: PC-0053 CIP
CURRENT APPLICATION NUMBER: US/10/079,111
CURRENT APPLICATION NUMBER: 09/232,160
PRIOR PLING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGram
SEQ ID NO 2
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     TYPE: DNA
ORGANISM: Homo sapiens
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Matches 2029; Conserv
 LENGTH: 2029
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Sequence 849, App
Sequence 853, App
Sequence 200, App
                                                                                                     September 15, 2004, 09:52:54; Search time 964 Seconds (without alignments) 10590.207 Million cell updates/sec
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             GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-907-841-200
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~ ^	GTCAGAA-GCTTGAAAGCAGGAAATCCGGATGTCTCGGTTATGAAGTGGAG 60 	QY 1081 CTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAA 	AG 1140 
<b>\</b> -	6-6	1141 CTGAAGTTTAGATGAGACAGAAATGAGGAG 	TC 1200    TC 1207
	121 CTGCCTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCA 180	1201	CC 1260     CC 1267
	181 CGATGGCCAGGTGCTTCAGCCTTGCTTCTCACTTCGACCACGAGGCTCC 240	1261	GAG 1320      GAG 1327
	241 IGGTCCAAGGCTCTTTGCGTGCAGAGACTTTCCATCCAGGTGTCATGAGAATTATGG 300 	QY 1321 AATGCCTTCTCTTATTGTAACCCTGCTGGATCCTATCTCCTACCTCCAAAGCTTCC  Db 1328 AATGCCCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCC	CC 1380     -   -  
		Qy 1381 CACGGCCTTTCTAGCCTGGCTATGTCCTAATAATALCCCACTGGGAGAAAGGAGTTTTGC  Db 1388 CACGGCCTTTCTAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGC	GC 1440     GC 1447
	SAAAG 4       SAAAG 4	OY 1441 AAAGTGCAAGGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGT	GT 1500    GT 1507
	CTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTTAGGA 48	OY 1501 CTGAGGCTAGGTGGAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATT	TT 1560     TT 1567
	ת ע	OY 1561 CCGCAGCTCAGACCCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTC	TC 1620    TC 1627
	TGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCA	Qy 1621 CTTCTGAGCCCGGTAAGAGCAAAAGAATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGA  1628 CTTCTGAGCCCGGTAAGAACAAAAGAATGGCAGAAAAGTTTAGCCCCTGAAAGGCCATGGA	GA 1680    GA 1687
		QY 1681 GATTCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCT 	CT 1740    CT 1747
	CAGAATTTATTGTCAGTGACAGTACTCGGTGGCATCCCCTTACTCTACAGACCTCCTCAGAATTTATTGTCAGTGACAGTACTCATTACTCAGTGACAGTACTCAGTGACTGAC	Qy 1741 GAGGATACGACAGTACACTGTCAGCAGGACTGTAAACACAGACAG	TT 1800     T 1807
	ATTGA	OY 1801 CTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACAC	GGTCT 1860         GGTCT 1867
	TITGIGICACAGAAGITITIAIGGAAACTAGCACCAIGICIACAGAAACIGAACCAITIG	Qy 1861 CTACCACTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAACAAAAATAAAAA DD 1868 CTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACAAAAAAAA	CT 1920      CT 1927
	TIGAAANTAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTC	OY 1921 CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTAC' DD 1928 CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATAC	ACTCAGT 1980         CTCAGT 1987
	1 TGCTAGTGCTTGCTCTCCTTCTTTGGTGCTGCAGCTGGTCTTTGAATTTTGGTAGTGTCA	QY 1981 AATTGTTTAAAAGTAATAAAATTCAACAAACATTTAAAAAAA 2025 	
	961 AAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAA 1020 	RESULT 3 US-09-833-381-853 ; Sequence 853, Application US/09833381	

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CTGAAGTTTAGATGAGACAGAAATGAGAGAGACACCTGAGGCTGGTTCTTTCATGCTC
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                                                          TTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTC
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  TITGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTG
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                                                                                                                  TGCTAGTGCTTGCTCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTTGCTATGTCA
                                                                                                                                        TGCTAGTGCTTGCTTCTTTTTTTGTGTGCTGCTGGTCTTTGGATTTTGCTATGTCA
                                                                                                                                                                        AAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAA
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROBISON, Keith E.
TITLE OF INVENTION: No. US20020132090Ale1 Nuc:
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT APPLICATION NUMBER: 09/516,448
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 833
LENGTH: 2404
                                                                                                                                                                                                                                              98.8%; Score 2005; Dilarity 99.7%; Pred. No. 0; Conservative 0; Mismatches
                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-09-833-381-853
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 2019; Conserv
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                                                                                                                                                                                                                                                                                                                         Score 1994; DB
Pred. No. 0;
0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR PAPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 200
LENGTH: 2372
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.8
Matches 1997; Conservative
                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-320-200
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennes
APPLICANT: Mather, Jennes
APPLICANT: Paoni, Jenses
APPLICANT: Paoni, Jenses
APPLICANT: Paoni, Jenses
APPLICANT: Paoni, Jenses
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timochy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: ApplicANT: Milliam, I.
ITILE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICANTON NUMBER: US/09/909,320
CURRENT APPLICANTON NUMBER: DAT/US00/04414
PRIOR FILING DATE: 2000-00-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR PRILING DATE: 1999-10-05
PRIOR PRILING DATE: 1999-10-05
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                                                                                            1928 CTTATAAATTTCTATTTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT
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Patent No. US20020132240A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Gao, Wei-Qiang
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781 GAAACTAGCACCATGTCTACAGAA 864 AATGAAGCTGCTGGGTTTGGAGGT	841 AArGAAGCTGCTGGGTTTGGAGGT 924 TTTGGTGCTGCAGCTGGTCTTGGA 	984 TTTACAAACAAGAATCAGCAGAAG 	1044 GCCAATGATAGCAACCTAATGAG 	1104 AAGAGTCCAAGCAAAACTACCGTC	1164 TGAGGAGACACACCTGAGGCTGGT 	1224 ATCAAAAGGGCCAAAGAACCAAAGAACCAAAGT	1284 TCAGACTGCCATTGGACTATGGA 	1344 CCTGTCTGGATCCTATCCTCCTAC	1404 GTCCTAATAATATCCCACTGGGAC	1464 TCATCAGTATCCAGTGGTAAAAAC 	1524 CAAGGAGTCACTGAGACCAAGGCT 	1584 GCTCTGAAAGAGAAACACGTATCC	1644 AGAATGGCAGAAAAGTTTAGCCCC	1704 TCTCTGTAAAGCTAAAATAAAGAA 	1764 GCAGGGACTGTAAACACAGACAGC 	1824 CACTGTTTAGAACACACACACTTR	1884 AGGAATATACTTTTACAAGTAA                 1861 AGGAATATACTTTTACAAGTAA

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PRIOR FILING DATE: 1999-12-20
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 200
LENGTH: 2372
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Best Local Similarity 99.8%;
Matches 1997; Conservative
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CORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: PCT/US99/30999
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
FILE REPRENENT: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT PELLING DATE: 2001-07-12
CURRENT PELLING DATE: 2001-07-12
FRIGR PELLING DATE: 2000-07-12
FRIGR PELLING DATE: 1999-07-06
FRIGR PELLING DATE: 1999-07-06
FRIGR PELLING DATE: 1999-07-06
FRIGR PELLING DATE: 1999-07-06
FRIGR APPLICATION NUMBER: US 60/146,222
FRIGR PELLING DATE: 1999-07-06
FRIGR APPLICATION NUMBER: US 60/146,222
FRIGR PELLING DATE: 1999-07-06
FRIGR APPLICATION NUMBER: PCT/US99/2054
FRIGR APPLICATION NUMBER: PCT/US99/2054
FRIGR APPLICATION NUMBER: PCT/US99/21090
FRIGR APPLICATION NUMBER: PCT/US99/21090
FRIGR APPLICATION NUMBER: PCT/US99/21090
FRIGR FILING DATE: 1999-00-13
FRIGR FILING DATE: 1999-10-05
FRIGR FILING DATE: 1999-11-29
FRIGR FILING DATE: 1999-11-29
FRIGR FILING DATE: 1999-11-29
FRIGR FILING DATE: 1999-11-20
FRIGR FILING DATE: 1999-11-20
FRIGR FILING DATE: 1999-11-30
                                                                                              2004 TICAACAACAITIAAAAAAA 2025
                                                                                                                                                                                                                 Sequence 200, Application US/09905291A
Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: BOESTEIN, DAVI
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Grimaldi, Christopher
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Hillan, Kenneth, J.
Kijavin, Ivar J.
Mither, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Gao, Wei-Qiang
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Qy 2004 TTCAACAATTTAAAAAA 2025	902-853-2 ence 200, ication N RAL INFOR LICANT: G	; APPLICANT: Ashkenazi, Avi ; APPLICANT: Botsteln, David ; APPLICANT: Desnoyers, Luc ; APPLICANT: Eaton, Dan L. ; APPLICANT: Ferrara, Napoleone		; APPLICANT: Gerritsen, Mary E. ; APPLICANT: Goddward, A. ; APPLICANT: Godowski, Paul J. ; APPLICANT: Grimaldi, Christopher J.	; APPLICANT: Gurney, Austin b. ; APPLICANT: Hillan, Kenneth, J. ; APPLICANT: Kljavin, Ivar J. ; APPLICANT: Mather, Jennie P.	; APPLICANT: Pan, James ; APPLICANT: Paoni, Nicholas F. ; APPLICANT: Roy, Margaret Ann ; APPLICANT: Stewart, Timothy A.	S T S	; TITLE OF INVENTION: Acids Encoding the Same ; FILE REFERENCE: 10466-11, ; CURRENT APPLICATION NUMBER: US/09/902,853 ; CURRENT FILING DATE: 2001-07-10	; PRIOR APPLICATION NUMBER: US/09/665,350 ; PRIOR FILING DATE: 2000-09-18 ; PRIOR APPLICATION NUMBER: US 60/143,048 ; PRIOR FILING DATE: 1999-07-07	; PRIOR APPLICATION NUMBER: US 60/145,698 ; PRIOR FILING DATE: 1999-07-26 ; PRIOR APPLICATION NUMBER: US 60/146,222 ; PRIOR FILING DATE: 1999-07-28	APPLICATION NUMBER: FILING DATE: 1999-05 APPLICATION NUMBER: FILING DATE: 1999-05	APPLICATION NUMBER: PCT/US99, FILING DATE: 1999-09-15 APPLICATION NUMBER: PCT/US99, FILING DATE: 1999-09-15	APPLICATION NUMBER: FILING DATE: 1999-1C APPLICATION NUMBER: FILING DATE: 1999-11	APPLICATION NUMBER: FILING DATE: 1999-11 APPLICATION NUMBER: FILING DATE: 1999-12	APPLICATION NUMBER: FILING DATE: 1999-12 APPLICATION NUMBER: FILING DATE: 1999-12	; PRIOR APPLICATION NUMBER: PCT/US99/30911 ; PRIOR FILING DATE: 1999-12-20 ; PRIOR APPLICATION NUMBER: PCT/US99/30999 ; PRIOR FILING DATE: 1999-12-20
Db 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGCT	961 TITACAAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAGTAAAGGAGGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	DD	Qy         1164         TGAGGAGACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCTGCCCAGCTGGGGAA         1223           Db         1141         TGAGGAGACACCTGAGGCTGGTTCTTTCATGCTCCTTACCTGCCCCAGCTGGGGAA         1200	QY 1224 ATCAAAAGGGCCAAAGAACCAAAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC 1283	OY 1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGCCCTTCTCCTTATTGTAAC 1343 Db 1261 TCAGGACTGCCATTGGACTGCACCACCAAGAGAATGCCCTTCTCCTTATTGTAAC 1320	OY 1344 CCTGTCTGGATCCTATCCTCCTAAGCTTCCCACGGCCTTTCTAGCCTGGCTAT 1403	OY 1404 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGACCTAAAACATC 1463 	Qy         1464         TCATCAGTATCCAGTGATAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC 1523           Db         1441         TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC 1500	QY 1524 CAAGGAGTCACTGAGACTTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA 1583	OY 1584 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1643 Db 1561 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1620	Qy 1644 AGAATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1703 	QY 1704 TCTCTGTAAAGCTAAAATAAAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA 1763 	QY         1764         GCAGGACTGTAAACACAGGCTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT         1823           DD         1741         GCAGGACTGTAAACACAGACTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT         1800	OY         1824 CACTGITIAGAACACACACACACATTACITITICIGGICICIACCACTGCTGAIAITITICIC         1883           DD         1801 CACTGITIAGAACACACACACACACTTITICIGGICICIACACTGCIGAIAITITICICI         1860	OY 1884 AGGAAATATACTTTTACAAGTAACAAAAACTCTTATAAATTTCTATTTTTATCT 1943 	Oy 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 2003 

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APPLICANT: WOLLY, WILLIAM: I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: 05/09/907,824
CURRENT FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US09/2094
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-14
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PRIOR PLING DATE: 1999-10-20
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-20
                      Sequence 200, Application US/09907824 Publication No. US20020197671A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  Godowski, Paul J.
Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Kljavin, Ivar J.
Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                                            APPLICANT: Genentech, Inc.
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US-09-907-824-200
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Pred. No. 0;
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 200
LENGTH: 2372
                                                                                                                                 Query Match
Best Local Similarity 99.8%;
Matches 1997; Conservative
                                                                       ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-824-200
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TITLE OF INVENTION: Secreted 1.

TITLE OF INVENTION: Secreted 1.

TITLE OF INVENTION: Acids Encoding the Same
FILE REPREMENTS: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,841

CURRENT PILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-2

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-2

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/2094

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

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98.3%; Score 1994; D:
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches
1981 TTCAACAACATTTGCTGAATA 2002
                                                                                                                                                             Sequence 200, Application US/09907841
Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                      Desnoyers, Luc
Eaton, Dan L.
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                                                                                                                                                                                                                                                                   1021 GCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCCGGAGAGGTCC 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1284 TCAGGACTGCCATTGGACTATGGAGTGCCACCAAAGAGAATGCCCTTCTCCTTATTGTAAC 1343
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                                                                                                                                                                                                                             GCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACTGATAAAAACCCAGAAGAGTCC
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     TTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT
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                                  TTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT
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AGCAGGGAAATCCGGATGTCTCGGTTATGAAGCAGGAGGAGTGTGAGCCTCAACATA GTTCCAGAACTCTCCATCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC CATCTGAGGTTTTCCCTGGCTCTGGATTATTGAGCATCTCCTCTTTATCCTTGCGTGC CATCTGAGGTTTTCCCTGGCTCTGAAGGGGTAGGCCAGGTGCTTCAGCCTG CATCTGAGGTTTTCCCTGGCTCTGAAGGGGTAGGCCAGGTGCTTCAGCCTG CATCTGAGGTTTCCCTCGACCACCAGGGCTCCTTGGCTGCTGGCTG	264 GAAGAGCTTTCCATCCAGGTGTCATGAGATTATGGGGATCACCCTTGTGAGCAAAAG 323 241 GAAGAGCTTTCATCAGGTGTCATGCAGATTATGGGGATCACCCTTGTGAGCAAAAG 323 241 GAAGAGCTTTCCAGGTGTCATGCAGAATTATGGGGATCACCCTTGTGACAAAAG 300 324 GCGAACCAGCAGAGTTCACAGAAGCTAAGGAGCCTGTAGGCTGCTGGGACTAAGG 301 GCGAACCAGCTGAATTTCACAGAAGCTAAGGAGCCTGTAGGCTGCTGGGACTAAGT 360 384 TTGGCCGGCAAGGACAAGTTGAAACAGCCTTGAAAGCTAGCT	AAAATGGGGTGGGTGTCCGATTTGGAAGGTTCCAGTGAGCCGAAGCCGAAGTTGCAGCCTATTTGAAGTTCCAGTGAGCCGACGTTTGCAGCCGACGTTTGCAGCCGACGTTTGCAGCCGACGTTTGCAGCCCTATTTGAAATGGAGCTTCCAGTTTGCAGCCCTATTTGTTTTTTTT		901 TITGCAACCGCTGCTCTGCTTTTTTTTTTTTTTTTTTTTT

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                                                                                                                                                         CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
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                                                                                                                                                                                                                                                                                                                                               GAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAG 300
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                                                                                                                                CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG
                                                                                                                                                                                                                   GEGITGCTICTCACTICCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA
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APPLICANT: Stewart, Timchy A.
APPLICANT: Tunas, Daniel
APPLICANT: Wead, Williams, P. Wickey
APPLICANT: Wood, Williams, P. Wickey
APPLICANT: Wood, Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT PRINC STATE 10466-14
CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT PRINC BARE: 2001-07-11
PRIOR PELICATION NUMBER: US/09/904,411
PRIOR PELICATION NUMBER: US/00/09-18
PRIOR PELICATION NUMBER: US/00/09-18
PRIOR PELICATION NUMBER: US/01/09/91
PRIOR PELICATION NUMBER: US/01/09/91
PRIOR PELICATION NUMBER: PCT/US9/2094
PRIOR PELICATION NUMBER: PCT/US9/2094
PRIOR APPLICATION NUMBER: PCT/US9/2099
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PRIOR APPLICATION NUMBER: PCT/US9/2099
PRIOR APPLICATION NUMBER: PCT/US9/2099
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US9/2099
PRIOR PELING DATE: 1999-10-05
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Pred. No. 0;
0; Mismatches 5;
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Best Local Similarity 99.8%;
Matches 1997; Conservative
                                                                                 Gerritsen, Mary E.
Goddard, A.
                                                                 Gerber, Hanspeter
                      Fong, Sherman
Gao, Wei-Qiang
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APPLICANT: ROY, MAGGARET AND
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APPLICANT: ROY, MAGGARET AND
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Modod, Williams, P. Wickey
APPLICANT: Wood, Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides
ITLE APPLICATION NUBBRE: POT/050/9120
PRIOR PLING DATE: 1995-00-02
PRIOR PLING DATE: 1995-00-03
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                   Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Filvaroff, Ellen
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ö 83 5 98.3%; Score 1994; D 99.8%; Pred. No. 0; ive 0; Mismatches Conservative Query Match Best Local Similarity Matches 1997; Conserv à

Length 2372;

DB 10;

; ORGANISM: Homo Sapien US-09-906-742-200

Sequence 200, Application US/09906742
Publication No. US20030023054A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Eaton, Dan L.

1164 11711 117	APPLICANT: Botstein, David ; APPLICANT: Botstein, David ; APPLICANT: Desnoyers, Luc ; APPLICANT: Eaton, Dan L. ; APPLICANT: Ferrara, Napoleone
1 ACCAGGAMATICCGANTOTTICOGATANTGAGGACTATGAGTTGAGCTCTACATAR 60  84 GITCCAGAACTCCCACCCGACTAGTTANTGACAACTCGCCTCTCANTGACCAGTGCT 123  12 CACTCGAGGATTTCCACCCGGACTAGTANTTGACAACTCGCCTCTCANTGACCAGTGCT 233  13 CACTCGAGGATTTCCACCCGGACTCTGAGGAGTAGGCAGATAGGCCAGGTTGCTTCCACCTGT 160  24 CACACCCGCACTTCCATCCGGCTCTGAGGAGTAGGCAGATAGGCCCAGGTTGCTTCGACCTG 160  25 CACACCCGCACTCATTCCATCCGGCTCTGAGGAGTAGGCAGATAGGCCCAGGTTGCTTCGACCTG 160  26 CATCGAGGATTCCACCGGGCTCTGAGGAATATAGGCAGATAGGCCCAGGTTGCTTCGACCTG 160  27 CACCCGCACTCCATCCACTCGACTCTGAGGAATATAGGCAGATAGGCCCAGGTTGCTTCGACCCAGGTTGCTTCGACCTG 160  28 CACCCGCACTCAATTCCACCGGGCTCTGAGGAATATAGGCAGATAGGCCCAGGTTGCTTCGACCCAGGTTGCTTCGACCTGTTGAGGCAGATAGTTGGACTGTTGAGGCAGATAGTTGGACTTGAGGCAGATAGTTGGACTTGAGGCAGATAGTTGGACTTGTTGAGGCACTTAGTTGGACTTGAGGCAGATAGTTGGACTTGTTGAGGCACTTAGTTGGACTTGTTGAGGCACTTTGAGGCAGTTGGAGGCAGATAGTTGGACTTGTTGAGACTTTGAGGAATATAGGCAGAATAGTTGGACTTGTTGAGACTTTGAGAATATTGAGAATTAGGCAGAATAGTTGGACTTTGAGAATTAGGAGAATTAGGCAGAATTAGGCAGAATAGTTGGACTTGTTGAGAATTAGGAGAATTAGGAGAATTAGGAGAATTAGGACACTTTGAGAATTAGGAGAATTAGGAGAATTAGGAGAATTAGGAGAATTAGGAGAATTAGGAGAATTAGGAATAGAATTAGGAGAATTAGGAGAATTAGGAGAATTAGGAGAATTAGGAGAATTAGGAGAATTAGGAATTAGGAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAAGAATTAGAAT	AGAGTCCAAGCAAACTACCGTGCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC

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                                                                                                                                                         APPLICANT: Kljavin, Kenneth, J.
APPLICANT: Kljavin, Yozu J.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, Jama Mather, Jennie P.
APPLICANT: Pan, Jama Mather, Jennie P.
APPLICANT: Pan, Jama J.
APPLICANT: Roy, Magazet Ann
APPLICANT: Roy, Magazet Ann
APPLICANT: Roy, Magazet Ann
APPLICANT: Roy, Magazet Ann
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, P.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT ELING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: US 0/143.04
PRIOR APPLICATION NUMBER: US 0/145.22
PRIOR APPLICATION NUMBER: US 0/145.22
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-18
PRIOR PRIOR PRIOR NUMBER: PCT/US99/2094
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Pred. No. 0;
0; Mismatches
                                                                                              Godowski, Paul J.
Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
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                                              Gerber, Hanspeter
Gerritsen, Mary E.
       Fong, Snermand.
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Best Local Similarity 99.8
Matches 1997; Conservative
                                                                                 Goddard, A.
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US-09-906-838-200
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AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCGGAGTGAGGCTCAACATA

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Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                         Goddard, A.
                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                          1141 TGAGGAGACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA 1200
                                                                                    1201 ATCAAAAGGGCCAAAGAACCAAAGAAAGTCCACCCTTGGTTCCTAACTGGAATCAGC 1260
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  TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA 1223
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                                                         1224 ATCARARGGCCCAAAGAACCAAAGAAGAAGTCCACCCTTGGTTCCTAACTGGAATCAGC
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Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, Avi
APPLICANT: Botstein, David
APPLICANT: Bestein, Lac
APPLICANT: Bestein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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ö Gaps o; Indels 5 98.3%; Score 1994; Dilarity 99.8%; Pred. No. 0; Conservative 0; Mismatches Similarity Query Match Best Local Simil Matches 1997; ( d 8

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	1404 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGACCTAAAACATC 1  1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGACCTAAAACATC 1  1381 GTCCTAATAATATCCCACTGGGAGAAAGGCTTTTGCAAAGTGCAAGGACCTAAAACATC 1  1464 TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTGGGTTGAAAGC 1	1501 CAAGGAGTCACTGAGACCAGGCTTTCTTACTGATTCCGCAGGTCAGACCCTTTCTTCA 1501 CAAGGAGTCACTGAGACCAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA 1584 GCTCTGAAAGGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1561 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1564 AGAATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	DD	1824 CACTGTTTAGAACACACACTTACTTTTCTGGTCTCTACCACTGCTGATAITTTCTCT	OY 1944 CADITACARAGARIACIAN CONTROLLAGIANTIGITTAAAAAGIAATAAAA 2003  1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGIAATTGTTTAAAAAGIAATAAAA 1980  QY 2004 TTCAACAACATTAAAAAAA 2025  Db 1981 TTCAACAAACATTGCTGAATA 2002	RESULT 14 US-09-907-942-200 i Sequence 200, Application US/09907942 i Publication No. US20030027146A1 i GENERAL INFORMATION: i APPLICANT: Genetech, Inc. i APPLICANT: Botstein, David i APPLICANT: Botstein, David i APPLICANT: Botstein, David i APPLICANT: Betstein, David i APPLICANT: Errara, Nau i APPLICANT: Errara, Napoleone i APPLICANT: Ferrara, Napoleone i APPLICANT: Fong, Sherman
		444 GGCTGGGTTGGAGATTCGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGG 503 421 GGCTGGGTTGGAGATTCGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGG 480 504 AAAATGGGGTGGTCTCTGATTTGGAGGTTCCAGTGAGCCGACAGTTGCAGCCTAT 563 [	TGTTACAACTCATCTGATACTTGGACTTGGTGCATTCCAGAAATTATCACCCCAAA  GATCCCATATTCAACACTCAACACAACA	*** **********************************	864 AATGAAGCTGCTGGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGCT	984 TTTACAAACAAGAATCAGCAAAGGAAATGATCGAAACCAAAGTAAAGAGAGAAGA 1043 961 ITTACAAACAACCAGAAAGAAATGATCGAAACCAAAGTAAAGGAGAAGA 1020 1044 GCCAATGATAGCAACCCTAATGAGGAATCAAGAAACTGATAAAAACCCAGAAGACCC 1103 1021 GCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACTGATAAAAACCCAGAAGAGTC 1103 1104 AAGAGTCCAAGGAAACTGACGGGGGATGCTGAAAACTGATAAAAACCCAAAGAGTC 1163 1104 AAGAGTCCAAGGAAACTGACGGGGGGGAAGAACTGATAAAAACCAAAGAGAGATC 1163 1104 AAGAGTCCAAGGAAACTGCCGGGCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140 1164 TGAGGAGACAACACCTGAGGCTGCGTTTTCATGCTCGTGAGCTTAGATGAGAACAGAAA 1120

Db 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	TSSACTITITITITITIES & CESTS & CENTRAL PORTION TO THE TOTAL PROPERTY OF THE PRO	121		scrrcrcacrrccarcrggaccacgaggcrccrggaggcrcrr	CATGCAGAATTATGGGGATCAC	Db 241 GAAGACTTTCCATCCAGGGTGTCATGCAGAATTATGGGGGATCACCCTTGTGAGCAAAAA	OF SERVICE A TITLE A CAGA A PAGA A CAGA CAGA CAGA CAGA CAG	301	ביי פוניקאיינייקנייקנייקנייקנייקנייקנייקנייקני	Qy 384 TTGGCCGGCAAGGACCAAGTTGAAACGAAGCTTGAAAGCTTTGAAACTTGCAGCTAT	Db 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCTTGAAAGCTTTGAAACTTGCA	Qy 444 GGCTGGGTTGGAGATTCGTGGTCATCTCTAGGATTAGCCCCAAACCCCCAAGT	Db 421 GGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGG	OV 504 AAAATGGGGGGGGGTGTCCTGATTTGGAAGGTTCCAGTGAGGTTCCACA		101	Qy 564 TGTTACAACTCATCTGATACTTGGACTAACTTGGATGCATTCCAGAAATTATCACCACAAA	Db 541 1GTTACAACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATTATCACCA	Qy 624 GATCCCATATTCAACACTCAAACTGCAACAACAACAAGAATTTATTGTCAGTGACAGT	DD 601 GATCCCATATTCAACACTCAAACTGCAACACAAACAACAAATTTATTGTCAGTG	Qy 684 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCTACTACTACTACTACTACTACTACTACTACTACTAC	Db 661 ACCTACTCGGTGGCATCCCCTTACTACTACTGCTGCCCCTACTACTACTACTACTACTACTACTACTACTACTAC	Qy 744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTCACAGAAGTTT	Db 721 CCAGCTTCCACTTCTATTCCAGGAGAAAAAATTGATTTGTGTCACAGAAGTTTTTATG	Qy 804 GAAACTAGCACCATGTCTACAGAAACTGAACCATTGTTGAAAAATAAAGCAGCATTCAAG	Db 781 GAAACTAGCACCATGTCTACAGAAACTGAAACTTGTTGAAAATAAAGCAGCAT	Qy 864 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTCCTCTTTC	Db 841 AATGAAGCTGCTGGGTTTGGAAGGTGTCCCCACGGCTCTGCTAGTGCTTGCT	Qy 924 TITIGGEGCTGCAGCTGGTTTTTTTTTTTTTTTTTTTTTTTTTT	Db 901 TTTGGTGCTGGTCTTGGATTTTGCTAAAAGTATGTGAAGGCCT	Qy 984 TITACAAACAAGAATCAGCAGAAATGATGATGGAAACGAAAGAGAGAG	Db 961 TTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAAGTAAGAAGAGAGG	Qy 1044 GCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACTGATAAAAACCCAGAAGGTCC	s 0; Qy 1104 AAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAAAAAAA	Db 1081	
	APPLICANT: Gerber, Hanspeter APPLICANT: Gerritsen Mary R		 APPLICANT: Gurney, Austin L. APPLICANT: Hillan, Kenneth, J.	APPLICANT: Kljavin, Ivar J. APPLICANT: Mather. Jennie P.	Pan, James	Paoni, Ni Roy, Marg	APPLICANT: Stewart, Timothy A. APPLICANT: Thumas. Daniel	APPLICANT: Williams, P. Mickey APPLICANT: Wood William I	. Z	OF INVENTION: Acids Encoding the Same CEFERENCE: 10466-14	CURENT APPLICATION NUMBER: US/09/907,942	PRIOR APPLICATION NUMBER: PCT/US00/04414		PRIOR FILING DATE: 1999-07-07 PRIOR APPLICATION NUMBER: US 60/145.698	FILING DATE	FILING DATE: 1999-0	PRIOR APPLICATION NUMBER: PCT/US99/20594 PRIOR FILING DATE: 1999-09-08		APPLICATION 1			PRIOR FILING DATE: 1999-10-05 PRIOR APPLICATION NUMBER: PCT/US99/28214		FRIOK FILING DAIE: 1999-11-50 PRIOR APPLICATION UMBER: PCT/US99/28564	APPLICATION N	APPLICATION PELLING DATE:	PRIOR APPLICATION NUMBER: PCT/US99/30911 PRIOR FILING DATE: 1999-12-20	PRIOR APPLICATION NUMBER: PCT/US99/30999 PRIOR FILING DATE: 1999-12-20	APPLICATION PILLING DATE:		LENGTH: 2372 TYPE: DNA	; ORGANISM: Homo sapiens US-09-907-942-200	98.3%; Score 1994; DB 10; Length 2372; Jarity 99.8%; Pred. No. 0;	Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps Ov 24 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTG		

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TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-4.

CURRENT APPLICATION NUMBER: US/09/904,859

FRICH APPLICATION NUMBER: 09/665,350

PRIOR APPLICATION NUMBER: POT/050/0414

PRIOR APPLICATION NUMBER: POT/050/0414

PRIOR APPLICATION NUMBER: BC7/050/0414

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PELING DATE: 1999-00-12

PRIOR PELING DATE: 1999-10-12

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PRIOR PELING DATE: 1999-10-12

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PRIOR PELING DATE: 1999-10-13

                                        Godowski, Paul J.
Grimaldi, Christopher
                                                                                      Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
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                                                                                                                                                                                                                                Roy, Margaret Ann
Stewart, Timothy F
Tumas, Daniel
Gerritsen, Mary E
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                                                   CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTAT
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                   ATCAAAAGGGCCAAAGAACCAAAGAAGAAGTCCACCTTGGTTCCTAACTGGAATCAGC
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            ORGANISM: Homo Sapien
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Sequence 200, Application US/09904859
Publication No. US20030036060A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fivaroff, Ellen
APPLICANT: Fivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
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US-09-904-859-200

1224 ATCAAAACGGCCAAAGAACCAAAGAAAGTCCACCCTTGGTTCCTAACTGGAATCAGC 1 1201 ATCAAAAGGGCCAAAGAACCAAAGAAAGAAAGTCCACCCTTGGTTCCTAACTGGAATCAGC 1 1201 ATCAAAAGGGCCAAAGAACCAAAGAAAGAAAGTCCACCCTTGGTTCCTAACTGGAATCAGC 1 1201 ATCAGACTGCCATTGGACTATGGAGTGCACCAAAGAAAAGAATGCCCTTCTCCTTATTGTAAC 1 1201 TCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGCCCTTCTCCTTATTGTAAC 1	0.00	Db 1441 TCATCAGTATCAGTAAAAAGGCCTCCTGGCTGTGAGGCTAGGTGGGTTGAAAGC 1500  Qy 1524 CAAGGAGTCACTGAGGCTTTCTCTACTGATTCCGAGCCTCAGACCTTCTTCT 1583	Qy         1644 AGAATGGCAGAAAAGTTTAGCCCCTGAAGCCATGGAGATTCTCATAACTTGGGACCTAA         1703           Db         1621 AGAATGGCAGAAAGTTTAGCCCCTGAAGCCATGGAGATTCTCATAACTTGGGACCTAA         1680           Qy         1704 TCTCTGTAAAGTAAATAAAGAAATAGAACAAGGCTGAGGATACGACGTACACTGTCA         1763           Db         1681 TCTCTGTAAAGTAAAATAAAAATAGAAGGCTGAGGATACGACAGTACACTGTCA         1740           Qy         1764 GCAGGGACTGAAAATAGAACACAGAGGCTGAAGGATTCGAACACAGTAGATTGGAAT         1823           Db         1741 GCAGGGACTGTAAACACAGACAGGCTCAAAGTTTTCTCTGAACACAATTGGAAT         1823           1741 GCAGGGACTGTAAACACAGACAGACCAAGGCTCAAAGCTTTTCTCTCTC	OY 1824 CACTGTTTAGAACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTT 1883  1801 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTT 1860  OY 1884 AGGAAATATACTTTTACAAGTAACAAAAATAAAAAAAATTTTTTTT		Search completed: September 15, 2004, 14:11:36 Job time : 973 secs
61 GTTCCAGAACTCCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120 144 CATCTGAGGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 203	264         GAAGAGCTITCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAA         323           241         GAAGACTTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAG         300           324         GCGAACCAGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGAGCTTAAGT         383			ACCTACTGGGGGGCATCCCCTTACTCTACAATACCTGCCCCTACTACTGCTCCTCCTGCT CCAGCTTCCACTTCTATTCCACGGAAAAAATTGATTTGTGTCCAGAAGTTTTATG CCAGCTTCCACTTCTATTCCACGGAAAAAAATTGATTTGTGTCACAGAAGTTTTTATG CCAGCTTCCACTTCTATTCCACGGAAAAAAATTGATTTGTTGTGTCACAGAAGTTTTTATG GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAAAAA	864 AATGAAGCTGCTGGAGTTTGGAGGTGTCCCCACGGCTCTGCTGGTGCTTGCT	984 TTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAG 1043

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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using sw model nucleic search, OM nucleic

September 15, 2004, 01:53:03; Search time B19 Seconds (without alignments) 10524.535 Million cell updates/sec Run on:

Title: Perfect score:

Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 segs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

N\_Geneseq\_29Jan04:\* Database

genesegn2001as:\* genesegn2001bs:\* geneseqn2003as:\* geneseqn2003bs:\* genesegn2003cs:\* geneseqn1980s:\* geneseqn2002s:\* genesegn2000s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Aa298172 Human sig Ade71445 Human cDN Ade71445 Human cDN Aax52250 Protein P Ad78520 Human PRO Af72408 Human PRO Ab7480 Human PRO Ab7480 Human PRO Ab7480 Human PRO Ab195576 Human ang Aca5960 Human PRO Aca5960 Human CDN Aca60164 Human cDN Aca60164 Human cDN Aca60164 Human cDN Aca60164 Human cDN Aca60164 Human cDN Aca60164 Human cDN Aca60164 Human cDN Aca60365 Novel hum Aca60365 Novel hum Aca60365 Novel hum Aca60365 Novel hum Aca60365 Novel hum Aca60368 CDNA enco
SUMMARIES	AAZ98172 ADE71449 ADE71449 ADE71449 AAX52250 AAX52250 AAX72408 AAX72408 ABL98087 ABL98087 ACA59060 ACA5960 ACA59166 ACD8154 ACA60164 ACA60164 ACA60164 ACA60164 ACA60166 ACA60166 ACA60166 ACA60166 ACA60166 ACA60166 ACA60166 ACA60166 ACA60166 ACA60166 ACA60166 ACA60166 ACA60166 ACA60166 ACA60166
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Length	2029 2023 2023 2023 2372 2372 2372 2372 2372
* Query Match	
Score	1
Result No.	222 222 232 232 233

Abx96181 Human sec	Aca05502 cDNA enco	Aca93699 Human cDN	Acd20169 Human sec	Aca67273 cDNA enco	Ach66246 Novel hum	Acd02300 Novel hum	Aca89291 Novel hum	Aca68928 Novel hum	Aca54972 Novel hum	Aca98450 Human PRO	Aca63375 cDNA enco	Acd19807 Human sec	Adb29405 Human sec	Adb17062 Human cDN	Ach03578 Human sec	Ada18261 Human sec	Acd66954 Human cDN	Adal9867 Novel hum	Adb17250 Human cDN	Acd83115 Human PRO	Ada16236 Human sec
ABX96181	ACA05502	ACA93699	ACD20169	ACA67273	ACH66246	ACD02300	ACA89291	ACA68928	ACA54972	ACA98450	ACA63375	ACD19807	ADB29405	ADB17062	ACH03578	ADA18261	ACD66954	ADA19867	ADB17250	ACD83115	ADA16236
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## ALIGNMENTS

RESULT 1

Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicorobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; muscular dystrophy; ss. Baughn MR; t, Hillman JL; Human signal peptide containing protein HSPP-64 cDNA SEQ ID NO:198. AAZ98172 standard; cDNA; 2029 BP. 98US-0090762P. 98US-0094983P. 98US-0102686P. 98US-0112129P. 99WO-US014484. (first entry) (INCY-) INCYTE PHARM INC. WO200000610-A2. 06-JAN-2000. -26-JUN-1998; 31-JUL-1998; 01-OCT-1998; Homo sapiens. 25-JUN-1999; 11-MAY-2000 11-DEC-1998; AAZ98172; AAZ981 

YT, Gorgone GA, Corley NC, Guegler KJ, Ba Au-Young J, Yue H, Patterson C, Reddy R, Tang YT, Akerblom IE, Bandman O; Lal P,

WPI; 2000-160673/14.

P-PSDB; AAY87287

New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease.

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                                                                                                                                                                                                                                                                                                                                                                                                       (including cancer), inflammation, causeases include cell prollieration reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma. Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP nucleic acids can be used for the recombinant production of HSPP nucleic acids can be used for the recombinant production of HSPP nucleic and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapetuics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    competitive drug screens, and for purification of HSPP from natural sources
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                                                                                                                      human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation
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                                                                               AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent
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    Page 288-289; 327pp; English
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GAGGATACGACAGTACACTGTCAGCAGGGACTGTAAACACAGAGAGGTCAAAGTGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated cDNA encoding a protein that is differentially expressed in breast cancer, designated PDEBC. The invention is useful to diagnose breast cancer. The invention is also useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of the disease. The present sequence represents cDNA encoding human PDEBC incyts 3044710CB1. Note: There are two sequences that have been assigned SEQ ID 2 in the specification, the present sequence represents the sequence given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
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                                                                                                                                                                                                                                      metastatic;
BP
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Best Local Similarity 100.0%; P.
Matches 2027; Conservative 0;
CDNA; 2027
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                                                                                                                                                                            Human cDNA encoding PDEBC
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1991	RESULT 4 AAX52250 ID AAX52250 ID AAX52250 ID AAX52250 ID AAX52250 ID AAX52250; XX XX AXC AAX52250; XX DT 25-UJN-1999 (first entry) XX DF 25-UJN-1999 (first entry) XX Collinger-Ellison syndrome; pastrointestinal ulceration; XX XX XX Congenital microvillus arrophy; skin disease; cell growth, abnormal keratinocyte differentiation; psoriasis; epithelial cancer; XW ADATINGER-Ellison syndrome; adstrointestinals; epithelial cancer; XW ADATINGON'S disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; XW Wound healing; tissue repair; ss. ADAR-1999 XX XX PN WO9914328-A2. XX PN WO9914328-A2. XX PN
303 ATCACCTTGTGAGCAAAAGGCGAACCAGCAGATTTCACAGAAGCTAAGGAGGC 360     301 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCTGAATTTCACAGAAGCTAAGGAGGC 360     302 ATCACCCTTGTGAGCAAAAAGGCGAACCAGATTTCACAGAAGCTTGAAAGGT 420     303 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACTGAAACACCTTGAAAGT 420     304 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACTGAAACACTTGAAACATTCAAAGGT 420     423 AGCCCAAACTTGCAGCTTGGGGAAAATGGGGTGGATTGGAACTTCCTAGGAT 482     481 AGCCCAAACTTGCAGCTTAGTGGGGAAAATGGGGTGGATTGGAAGTTCCTAGGAT 602     481 AGCCCAAACTTGCAGCTTAGTTGAACTCATCCTGATTTGGACTTACTCCTAGGAT 602     481 AGCCCAAACTTGCAGCTTAGTTGAACTCATCATCATACTCGTAGCTTCCTAGGATT 602     481 AGCCCAAACTTTGTACACCTCATTTCAACACTCCTAACTCGTGCATT 602     481 AGCCCAAATTATCACCACCAAGTTGTTACAACTCAAACTCCTGATT 602     481 AGCCGAAATTATCACCACCAAGTTGTTAAACTCCTAAACTCGTAACTCGTGCATT 602     481 AGCCGAAATTATCACCACCAAGTTGTACAACTCAAACTCCTAACTCGTGCATT 602     481 AGCCGAAATTATCACCACCAAGTTCCAATTCCAAACTCCTAACTCGTGCATT 602     481 AGCCGAAATTATCACACCAAGATCCCATCATCTAAACTTCCAAAAAAAA	963 AGGTATGTGAAGGCCTTCCCTTTACAACAAGAATCAGCAGAAGGAAATGATCGAAACC 1022  961 AGGTATGTGAAGGCCTTCCCTTTTACAACAAGAATCAGCAGAAGGAAATGATCGAAACC 1020  1023 AAAGTAGTAAAGGAGAGAAAGGCCAATGATGGCAGAAGGAAATGATCGAAACC 1020  1021 AAAGTAGTAAAAGGAGAGAGAGCCAATGATGAGCAAACCTAATGAGGAAACT 1082  1021 AAAGTAGTAAAAAGGCCAATGATAGCAAACCCTAATGAGGAAACT 1080  1083 GATAAAAAACCCAGAAGGAGAGAGCCAATGATGAGCAAACCTAGGAAACT 1140  1143 GAAGTTTAGATGAGAGAGTCCAAGAGAAACTACCGTGCGATGCCTGGAAGCT 1140  1143 GAAGTTTAGATGAGAGAGTCCAAGAGAAACCCAAGGAAACTTCTTTCATGCTCCT 1202  1141 GAAGTTTAGATGAGAAATGAGGACACACCTGAGGCTGGTTTCTTTC

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323 300 360 443 420 503 480 563 540 623 900 683 99 743 720 803 780 863 923

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PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract
                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
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Pred. No. 0;
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                                                                                                                                                                                                                         Matches 1997; Conservative
                                                                                                                                                                                                         Local Similarity
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970S-0059119P.
970S-0059121P.
970S-0059124P.
970S-0059184P.
970S-0059266P.
970S-0062125P.
970S-0062128P.
970S-0062287P.
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27-001-1997;
28-001-1997;
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28-001-1997;
28-001-1997;
29-001-1997;
29-001-1997;
29-001-1997;
                                  17-SEP-1997;
18-SEP-1997;
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18-OCT-1997;
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                        901 TTTGGTGCTGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT
                                                             TTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACCAAAGTAGTAAAAGGAGGAGAAG
                                                                                                                                                                                          1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA
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                                                                                                                  1044 GCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACTGATAAAAACCCAGAAGAGTCC
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The invention relates to a novel nucleic acid encoding a PRO polypeptide. The polypeptides and polynucleotides of the invention may be useful as research tools and as therapeutics for treating enterocolitis, Zollinger-Blison syndrome, gastrointestinal ulcerating, providasis, carcer, Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal scarting and wound healing, nerve repair, thrombosis, bone and/or actiage formation, angiogenesis, asthma, rheumatoid archritis, multiple sclerosis, inflammatory disorders, atherosclerosis, cardiac injury, infertility, premature aging, AlDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinflamatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; vasctropic; chemotaxic; anglogenic; neuroprotective; vastropic; chemotaxic; antiarthritic; antiinflumatic; antiarthritic; antiinflumatic; antiarteriosclerotic; cardiant; antidabetic; cerebroprotective; thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease; Alzheimer's; ALS, neuropathy; dermal scarring; wound healing; nerve repair; thrombosis; bone; cartilage formation; angiogenesis; asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder; atherosclerosis; cardiac injury; infertility; premeture aging; AlDS; diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.
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                                           1981 TTCAACAAACATTTGCTGAATA 2002
                                                                                                                                                                                                                                                                    BP.
2004 TTCAACAACATTTAAAAAAA
                                                                                                                                                                                                                                                                ADC78520 standard; cDNA; 2372
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Best Local Similarity 99.8
Matches 1997; Conservative
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The present sequence is one of sixty one nucleic acids encoding novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple solerosis), infertility, AlDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization
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antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation; ss.
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99.8%; Pred. No. 0;
:ive 0; Mismatches
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99WO-US02813.
99WO-US028654.
99WO-US028656.
99WO-US030991.
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99US-0145698P.
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Best Local Similarity 99.8
Matches 1997; Conservative
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P-PSDB; AAB80247.
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Filvaroff E, F
Godowski PJ, G
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20-DEC-1999;
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Williams PM
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                                                                                           GAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAG
                                                                                                                                                       GCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGTGGGGGCTGTAGGCTGGGGCTGAAGT
                                                                                                                                                                                                     TTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCTTTGAAAAGCTTTGAAAACTTGCAGCTAT
CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG
                                                                    Grennectronactrocarchedaccaceacercchegrecaagecronance
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                                                                                                                                          GCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT
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in chromosome and
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25-APR-2000; 2000US-0199397P.
22-MAY-2000; 2000US-0199397P.
05-JUN-2000; 2000US-02014042.
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99WO-US021090.
99US-0169495P.
99US-0170262P.
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18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
22-FEB-2000; 2000WO-US004414.
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Gaps

modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis.

New isolated secreted and transmembrane PRO polypeptide useful for

WPI; 2002-731348/79

P-PSDB; ABG95853

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98US-008811P-
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98US-0088825P-
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Godowski PJ; Goddard A, Wood WI; Gerritsen ME, Watanabe CK, Filvaroff E, C, Gurney AL, (GETH ) GENENTECH INC. Eaton DL, Fi Grimaldi JC,

CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCCACGATGGCCAGGTGCTTCAGCCTG 203

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GIGITGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 263 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240

CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG

143 83 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC GITCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC Gaps 0; DB 6; Length 2372; Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other; 5; Indels 0; Mismatches Score 1994; Pred. No. 0; 2; Fig 5; 399pp; English 98.3**%**; 99.8**%**; Matches 1997; Conservative Query Match Best Local Similarity 84 61 Claim ð ď à qq

1312   CTICTORATANTATICCACTICGANGGTTTTCCANGGCCTTTCTNGCCTGANGTT 1380   1404   GTCCTNATRATATICCACTICGANGANGTTTTCCANGGCCTTTCTNGCCTTGANGANGTTTTCCANGGCCTTTCTTANGANGTTTTCCANGGCCTTTCTTANGANGTTTTCCANGGCTTTCTANGANGTTTTCCANGGCTTTCTANGANGTTTTCCANGGCTTTCTANGANGTTTTCCANGGCTTTCTTCTTCTTTCTTCTTCTTCTTCTTCTTCTTCTT	RESULT 9 ABL88087 ID ABL88087 standard; CDNA; 2372 BP. XX AC ABL88087; XX AC ABL88087; XX DT 16-MAY-2002 (first entry) XX B Human PRO263 CDNA sequence SEQ ID NO:31. XX Wulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; XX XX XX Wulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; XX XX XX XX XX XX XX XX XX XX XX XX XX
24 GAAGACTTTCCATCCAGGTGCATGCAGATTATGGGGATCACCCTTGTGAGCAAAAG 323 24 GAAGACTTTCCATCCAGGTGTCATGCAGATTATGGGGATCACCCTTGTGAGCAAAAG 320 324 GAAGACCTTTCCATCCAGGTGTCATCAGATTATGGGGATCACCCTTGTGAGCAGAAAAG 320 325 GCGAACCAGCAGCAGCAGATTCACAAAACCTAGAGGGCTTGAGCTTGAAACTTGAGCACTAAGT 330 326 GCGAACCAGCAGCAGCAGAATTCACAAAACCTCTGAAGCTTGAAACTTGAGCTAAGT 340 327 TTGGCCGGCAAGGACCTGAATTTCACAAAACCTCTGAAGCTTTGAAACTTGCAGCTTAAGT 340 328 TTGGCCGGCAAGGACCAAGTTGAAACACCTTGAAAGCTTGAAACTTGCAGCTTAAGT 340 444 GCCTGGGTTGGAATTTCACAAAACCCTTGAAACTTGAAACTTGCAGCTTAAAATTGCACCCAAATTGAAACTTGGAACTTGAAACTTGCAGCTTAAAAATTGCACCCAAATTGAAACTTGGAACTTTGAAACTTGCAGATTTACAACCCCAAATTGAAACTTGGAACTTTGAAACTTGCAGATTTACAACCCCAAATTTACAACTTCAAATTTGAAACTTGAAACTTGAAACTTGAAACTTGAAAATTAACACCCAAAATTAACTTGAAACTTGAAACTTGAAAAATTAACACACAAAATTAACAAAAAAAA	984 TTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGAGAGGAGAGAGA

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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, theumatoid arthritis, angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides thrombophlebitis, lymphangitis, tumour healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping, ABL88259 to ABL88267 represent primers and probes used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
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Gurney AL, Hillan KJ, Marsters SA, Pan J,
Watanabe CK, Williams PM, Wood WI, Ye W;
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Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; gene; ss.
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2001WO-US017443.
2001WO-US017800.
2001WO-US019692.
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BAKER K P.
FERRARA N.
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
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GERRITSEN M E.
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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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PAONI
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                                                                                                                         The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver cardinoma) and wound healing. The present sequence is a coding sequence of the invention
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                                One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
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Best Local Similarity 99.8%; Pred. No. 0;
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   1884 AGGAAATATACTITTACAAGTAACAAAAAAAAAACTCCTTATAAATTTCTATTTTTATCT
                                  GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA
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## (GETH ) GENENTECH INC.

Ferrara N; ME, Goddard A; i A, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F F, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard FJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; P, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; PM, Wood WI; Ashkenazi A, Filvaroff E, Williams PM, Mather JP, Godowski

WPI; 2003-328338/31. P-PSDB; ABU71625.

Isolated nucleic acid useful for e.g., treating pathological disorders encodes a secreted or transmembrane protein.

Claim 2; Fig 73; 473pp; English.

The invention relates to human PRO polypeptides (secreted or transmembrane polypeptides) and the polymucleotides encoding them. The PRO polypeptides and polymucleotides can be used in treating pathological disorders and tumours, in therapeutic treatment of cardiac insufficiency disorders and in therapeutic treatment of disorders involving protein secretion by the pancreas, including diabetes. They can also be used in treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, and skin diseases associated with abnormal keratinocyte differentiation (e.g., psoriases, epithelial cancers such as lung

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TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCCTGCCCAGCTGGGGAA
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 squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas). The sequences can be used as molecular markers for protein electrophoresis purposes and can be utilised in protein-protein binding assays, biochemical screening assays, immunoassays and cell-based assays. This sequence represents a human PRO polynucleotide of the invention
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                                                                                                                                  Gaps
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0
                                                                                                         7; Length 2372;
                                                                                Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
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                                                                                                      Score 1994; DB
Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.8%;
Matches 1997; Conservative
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Human, secreted and transmembrane protein, PRO polypeptide, cancer,
Alzheimer's disease, ischaemia, cytostatic, nootropic, vasotropic,
neuroprotective, gene, ss.
                                                                                                            cDNA encoding human PRO polypeptide #36.
1981 TTCAACAACATTTGCTGAATA 2002
                                               ACA58457 standard; cDNA; 2372 BP
                                                                                                                                                                                                                                                                                                                                            9705-0062125P-
9705-0062185P-
9705-0062814P-
9705-0063141P-
9705-0063120P-
9705-0063121P-
9705-0063121P-
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97US-0059117P.
97US-0059119P.
97US-0059121P.
97US-0059122P.
97US-0059124P.
97US-0059263P.
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                                                                                      10-JUN-2003 (first entry)
                                                                                                                                                                                           US2002192659-A1.
                                                                                                                                                                        Homo sapiens.
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17-0CT-1997;
21-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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31-OCT-1997
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                                                                    ACA58457;
                                       ACA58457
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New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                  Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 73; 474pp; English.
                                                                                                                                                                                          05-JAN-2000; 2000WO-US000219.

11-FEB-2000; 2000WO-US000219.

12-FEB-2000; 2000WO-US006414.

24-FEB-2000; 2000WO-US006414.

02-MAR-2000; 2000WO-US005841.

30-MAR-2000; 2000WO-US008413.

30-MAR-2000; 2000WO-US014042.

22-MAY-2000; 2000WO-US014042.

23-JUL-2000; 2000WO-US015264.

28-JUL-2000; 2000WO-US015264.
                                                                  99WO-US020944
99WO-US021090
99WO-US0213089
99WO-US028214
99WO-US028313
99WO-US02856
99WO-US028565
99WO-US030995
                                      98WO-US019437.
98WO-US025108.
99WO-US020594.
         98WO-US018824
98WO-US019177
                             98WO-US019330
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                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-361832/34.
P-PSDB; ABU71480.
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The present invention relates to the isolation of novel human secreted and transmembrane proteins (PRO polypeptides), and the polynucleotide sequences are useful in sequences encoding them. The polynucleotide sequences are useful in molecular biology, as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide sequences may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or their antibodies are useful in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as cancer, Alzheimer's disease or ischaemia, and in various diagnostic assays. The present sequence encodes a human PRO polypeptide of the invention

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

98.3%; Score 1994; DB 7; Length 2372; 99.8%; Pred. No. 0; iive 0; Mismatches 5; Indels 0; Gaps Query Match Best Local Similarity 99.8 Matches 1997; Conservative

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	1284 TCAGGACTGCATTGGACTATGGAGTGCACCAAAGAGAATGCCTTCTCTTATTGTAAC 1284 TCAGGACTGCCATTGGACTATGGAGTGCAAAGAGAATGCCCTTCTCTTATTGTAAC 1261 TCAGGACTGCCATTGGACTATGGAGTGCAAAGAGAATGCCCTTCTCCTTATTGTAAC	1344 CCTGTCTGGATCCTACCTCCCAACGCTTCCCACGGCCTTTCTAGCCTGGCTAT	1404 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGACCTAAAACATC 1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGACCTAAAACATC	1464 TCATCAGTATCCAGTGGTAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC	QY 1524 CAAGGAGTCACTGAGACCTITCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA 1583	GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 	OY 1644 AGAAIGGCAGAAAAGTITAGCCCCTGAAAGCCAIGGAGAITCTCATAACTIGAGACCTAA 1703	1704 TCTCTGTAAAGCTAAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCA 1681 TCTCTGTAAAGCTAAAATAAAGAATAGAACAAGGCTGAGGATACGACAGTACACTGTCA	OY 1764 GCAGGACTGTAAACACAGACTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT 1823	1824 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1801 CACTGTTTAGAACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT	OY 1884 AGGAATATACTITTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTTTTATCT 1943	OY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAAAA 2003 	Oy 2004 TTCACAACATTTAAAAAA 2025 	RESULT 13 ACA60164 ID ACA60164 standard; cDNA; 2372 BP.	XX ACAG0164; XX DT 12-JUN-2003 (first entry)	XX DE Human cDNA for secreted/transmembrane protein PRO263. XX XW Human; ss; gene; secreted protein; transmembrane protein; PRO; XW gene therapy; chromosome identification; chromosome marker. XX
84 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143	CTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGGCCTG  TTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA  TTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA  TTGCTTCTTCATCTTCAATCTAGAACCAAGAGCTCTTTCAAGGCTCTTTGCGTGCAAGGCTTCTTTGCGTGCAAGAACCTTTTGCGTGCAAGAACTAGAAACAAAAAAAA	GLGITGCITCLATTCCATCTGGACCACGAGGGTCCTGGTCCAGGGCTGGAGGGTTACCATCCAGGGTCTATGGAGATTATGGGGATCACCCTTCGAGGGTCTATGGAGAATTATGGGGATCACCCTTCGAAAGGCTTTCCATCCA	324 GCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCGGACTAAGT 383 	ACCAAGTTGAAACAGCCTTGAAAGCTAGCTTT 	GTGGG       GTGGG	504 AAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 563 	564 IGTTACAACTCATCTGGACTAACTCGGGCATTCCAGAAATTATCACCACAAA 623 	624 GATCCCATATTCAACACTCAAACTGCAACACAACAACAACAATTTATTGTCAGTGACAGT 683 	684 ACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCCTACTACTACTCCTCCTCCT 743	CCAGCTTCCACTTCTATTCCACGGGAAAAAAATTGATTTGTGTCACAGAAGTTTTTATG	804 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAG 863 	864         AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGCT	924 TTTGGTGCTGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT 983 	984 TITACAAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAAG 1043 	1044 GCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAAGAGTCC 1103 	1104 AAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1163 

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9705-0063541P.
9705-0063544P.
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9705-0063564P.
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9705-0063564P.
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98WO-US019330.
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99WO-US028565
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Homo sapiens.
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17-OCT-1997;
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The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of a secreted/transmembrane polypeptides, or PRO polypeptides or a encoding a PRO protein extracellular domain. Also included are a vector comprising the PRO protein extracellular domain. Also included are a vector comprising to polypeptide (by culturing the host cell for the expression of the PRO polypeptide, and recovering the PRO polypeptide (having at least 80% sequence identity to: (a) an isolated PRO polypeptide (having at least 80% sequence identity to: (a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino acid sequence selected from the 61 PRO proteins; (b) an amino acid sequence selected from the 61 PRO proteins; (b) an amino acid sequence anotelic acid molecule deposited with an ATCC number (detailed in the specification); or (c) an extracellular domain of a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a PRO polypeptide or to a proper protein a sample suspected of containing the polypeptide. In the protein a proper protein a proper protein a proper protein a proper protein and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides and nucleic acids may also be used in tissue a protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO putipodies are useful in diagnostic assays for PRO, and the isolated sources. The present sequence encodes a PRO protein electrophoresis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, in generating probes and in tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                              , Botstein D, Desnoyers L, Eaton DL, Ferrara N; , Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; , Wood WI;
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         20-DEC-1999; 99W0-US33099; 20-DEC-1999; 99W0-US330999; 05-JAN-2000; 2000W0-US303565; 22-FEB-2000; 2000W0-US303565; 24-FEB-2000; 2000W0-US308414; 20-MAR-2000; 2000W0-US30841; 22-MAR-2000; 2000W0-US3084139; 22-MAY-2000; 2000W0-US301564; 28-JUL-2000; 2000W0-US301564; 24-AUG-2000; 2000W0-US33328;
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Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

0; Gaps 98.3%; Score 1994; DB 7; Length 2372; 99.8%; Pred. No. 0; 11ve 0; Mismatches 5; Indels 0; Best Local Similarity 99.8 Matches 1997; Conservative Query Match

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cirrhosis, fibrosis, restenosis, dermal fibrotic condition, keloid, scarring, ischaemia, stroke, hypertension, heart attack, atherosclerosis, infertility, gene therapy, gene; ss.
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9705-0059117P

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99WO-US028313
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                                                      US2002197671-A1
                                    Homo sapiens.
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The invention describes a new isolated nucleic acid molecule comprising
the full length coding sequence of the DNA deposited with the American
Type Culture Collection (e.g. ATCC Deposit No. 209288), or a sequence
with at least 80% identity to a DNA encoding a PRO polypeptide comprising
any of 61 sequences having 164-1119 amino acids fully defined in the
specification. The PRO polypeptides or polynucleotides are useful as
the parameteristic disposites, biosensors or bioreactors. These are
comparamenticals, diagnostics, biosensors or broreactors. These are
particularly useful for detecting or treating e.g. Parkinson's disease,
comparaticularly useful for detecting or treating e.g. colorectal
cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
crestenosis, dermal fibrotic conditions (e.g. keloids or scarring),
cischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
cischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
cischaemia, strokes, hypertension, heart attacks, attherosclerosis, or
infertility in mammals (e.g. humans), dogs, cats, cattle, horses, sheep,
complexence of these diseases. The PRO polypeptides are asfold
as molecular weight markers, or for chromosome identification. The PRO
genes are useful as hybridisation probes, or for screening libraries of
therapy, particularly for replacing a defective gene. This sequence
concepts a novel human secreted and transmembrane PRO polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO335), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
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                                                                                                                                                                                                                          ; 2000WO-US007377.
; 2000WO-US008439.
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; 2000WO-US015264.
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2000WO-US000219.
2000WO-US003565.
2000WO-US004414.
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The invention describes an antibody that specifically binds to a PRO polypeptide having a fully defined amino acid sequence given in the specification. The antibody is useful in identifying PRO polypeptides useful for various industrial applications, including pharmaceuticals, affinity purification of PRO polypeptides from recombinant cell culture or natural sources. The antibody is also used for antagonists, may be used for preparing a medicament for its agonists or antagonists, may be used for preparing a medicament for diagnosing or treating a condition responsive to the antibody, PRO polypeptide, or its agonists. This sequence encodes a novel human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                                                                            New antibody useful for identifying PRO polypeptides, for affinity purification of PRO polypeptides, and for preparing a medicament for polypeptide or treating conditions responsive to the antibody or PRO polypeptide.
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Wood WI;
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Watanabe CK,
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P-PSDB; ABU90878.
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Grimaldi J
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Godowski PJ;

Gaps .; Length 2372; Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other; Indels 'n, Score 1994; DB 7; Pred. No. 0; Mismatches · 0 98.3**%**; 99.8**%**; Best Local Similarity 99.8 Matches 1997; Conservative Query Match δ

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              GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC
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GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC
                                                                                                      CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG
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1020 1103 1200 1283 TTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAG 1043 1223 1403 1560 1583 540 623 900 683 099 743 720 803 780 863 840 900 983 960 923 TGTTACAACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACAAA TGTTACAACTCCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATTATCACCCCAAA CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTCACAGAAGTTTTATG GCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACTGATAAAAACCCAGAAGAGTCC AAAAATGGGGTGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT GATCCCATATTCAACACTCCAACACACAAACAACAACAGAATTTATTGTCAGTGACAGT CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTGTCACAGAAGTTTTTATG GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAG GCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACTGATAAAAACCCAGAAGAGTCC ACCTACTCGGTGGCATCCCCTTACTACAATACCTGCCCCTACTACTACTACTCCTCCTGCT ACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCCTACTACTACTCCTCCTGCT GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAG Tricgrecrecrecrecricerringearringerarcreanagerrargaagecerrecer AAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA AAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCTGAAGTTTAGATGACAGAAA TTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA TGAGGAGACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA ATCAAAAGGGCCAAAGAACCAAAGAAGAAGTCCACCCTTGGTTCCTAACTGGAATCAGC CCTGTCTGGGATCCTATCCTCCTCCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTAT GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGACCTAAAACATC TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA ATCAAAAGGGCCAAAGAACCAAAGAAGAAGTCCACCTTGGTTCCTAACTGGAATCAGC TCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGCCCTTCTCCTTATTGTAAC CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTAT GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGACCTAAAACATC TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC 564 1021 1081 624 601 684 661 744 721 864 924 1044 1104 1164 1141 1224 1201 1284 1261 1344 804 781 901 984 196 1321 1404 1381 1464 1441 ð g ₽ ద à g à 셤 à Оp ð g ò g ò 임  $\delta$ 염 à g δ qq ò q ठ g ò qq d qq  $\dot{\circ}$ ð à qq

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GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAAAAA	1944
AGGAAATATACTITTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTTATCT	1861
AGGAAATATACTITTACAAGTAACAAAAAAAAACTCTTATAAAAATTTCTATTTTTTATCT	884
CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT	801
CACTGITIAGAACACACACACATACITITICIGGICTCTACCACTGCTGATATITICICT	824
GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT	1741
GCAGGGACTGTAAACACAGGCCAAAAGTGTTTTCTCTGAACACATTGAGTAT	1764
TCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGGTACGACAGACA	1681
TCTCTGTAAAGCTAAAATAAAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCA	1704
AGAATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1621
AGAATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1644
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1620 1703 1680 11740 11860 1920 1920	GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA  AGAATGGCAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA  AGAATGGCAGAAAAGAAA

Search completed: September 15, 2004, 07:40:48 Job time : 835 secs sec sec hum hum hum hum hum PRO PRO

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Human; cytokine; cell proliferation; cell differentiation; growth factor;
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27-APR-2000; 2000US-00560875.
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ABB11979
 -WODEL-frame+ n2p.model -DEV=xlp
-Q=/Cgn2_1/USPTO spool p/US10079111/runat_13092004_102125_1809/app_query.fasta_1.2183
-Q=/Cgn2_1/USPTO spool p/US10079111/runat_13092004_102125_1809/app_query.fasta_1.2183
-Q=/Cgn2_1/USPTO spool p/US10079111/runat_13092004_102125_1809/app_query.fasta_1.2183
-LCOPEXT=0 -UONTS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -TRR MIN=0 -ALIGN=15
-MODB=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRE-SI30079111 @CGN 1 1 308 @vunat 1 3092004 102125_1809 -NCPU-6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPE -DELEXT=7
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Adc78521
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                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                                                                                   using frame_plus_n2p model
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                                                                                                                                                                                                                                        Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the nucleotides.

CC introduction of the invention, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although movel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, sense cell growth factor activities, and hence confidence of chemotactic or chemotactic activities, thromboly.

CC differentiation activities, receptor or inhibin-related activities; information activities, activities, takemactopic or chemotactic or chemotactic activities, activities, takemactopic or chemotactic or chemotactic activities, activities, takemactopic or chemotactic or chemotactic activities, activities, activities, activities, incombination are useful for preventing, treating or metastasis.

C bepending on their biological activities, polypeptides and nucleotides of the inventions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include activities activities and about a strain cornelic acids encoding them) may be used to promote wound careating (e.g., of promote wound careating (e.g., of actoprores), chronic inflammatory conditions (e.g., asthma or arthritis), arterial isoname, bound and inflammatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.

Polypeptides with growth factor activity may be used in the treatm
                                                                                                                              Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GlyThrMetAlaArgCy8PheSerLeuValLeuLeuThrSerlleTrpThrThrArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           screening techniques. The present sequence represents a novel human polypeptide of the invention
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Matches:
Conservative:
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                                                                                                                                                                                                                20; Page 291; 1963pp; English.
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1772.00
100.00%
99.71%
49.17%
                                                     Liu C, Drmanac RT;
                                                                                       2001-457740/49
                  HYSE-) HYSEQ INC
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                                                                                                         N-PSDB; ABA09223
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                                                            ATGGGGATCACCCTTGTGAGCAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAG
                                                                                                                                                                                                                      AAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCT
                                                                                                                                                                                                                                                 LysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSer
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                                                                                                                                             GAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTG
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Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
enterocolitis;
protein; transmembrane protein; human;
Secreted
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Homo sapiens

WO9914328-A2

98WO-US019330 16-SEP-1998;

17-SEP-1997; 17-SEP-1997; 17-SEP-1997;

9705-0059115P 9705-0059119P 9705-0059121P 9705-0059122P 9705-0059184P 9705-0059263P 9705-0062125P 9705-0062285P 9705-0062287P 9705-0063286P 9705-006386P 9705-0063886P 17-SEP-1997 17-SEP-1997 17-SEP-1997

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9705-0063045P 9705-0063121P 9705-0063121P 9705-0063127P 9705-0063328P 9705-0063541P 9705-0063542P 9705-0063542P 9705-0063542P 9705-0063543P 9705-0063738P 9705-0063734P 9705-0063734P 9705-0063738P 9705-0063738P 9705-0063738P 9705-0063738P 9705-0063738P 9705-0063738P 9705-0063738P 9705-0063738P 9705-0063738P 9705-0064208P 9705-0064208P 9705-0064208P 9705-0064208P 28-OCT-1997 28-OCT-1997 28-OCT-1997

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97US-0066466P. 97US-0066511P. 97US-0066770P. 97US-0066364P. 97US-0066453P. 97US-0066772P 97US-0066840P 24-NOV-1997 25-NOV-1997 24-NOV-1997

(GETH ) GENENTECH INC

Yuan J; ٦, Chen Pennica D, Goddard A, Gurney AL, WPI; 1999-229533/19. N-PSDB; AAX52250. Wood WI,

ŏ New isolated human genes and polypeptides used in, e.g. treatment gastrointestinal ulceration.

Claim 12; Fig 74; 320pp; English

Antistatives represent becreted and trainsender number procession.

CDNA sequences are obtained from CDNA libraries, prepared from fetal

concoded polypeptides have specific uses based on their homology to known

polypeptides. e.g. PRO211 and PRO217 can be used for disorders associated

with the preservation and maintenance of gastrointestinal mucosa and the

colypeptides. e.g. PRO211 and PRO217 can be used for disorders associated

with the preservation and maintenance of gastrointestinal uncosa and the

collinger-Ellison syndrome, gastrointestinal ulceration and congenital

microvillus atrophy, skin diseases associated with abnormal keratinocyte

differentiation (e.g. psoriasis, epithelial cancers such as lung squamous

cell carrinoma of the vulva and gliomas), potent effects on cell growth

can development, diseases related to growth or survival of nerve cells

including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or

cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal

cancer. PRO265 can be used as a for fibromodulin, e.g. for reducing dermal

cancer. PRO265 can be used as a for fibromodulin, e.g. for reducing dermal

cancer used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can

be used as an anti-thrombotic agent; PRO287 polypeptides and portions may

have therapeutic applications in wound healing and tissue repair; PRO317

can be used for treating problems of the kidney, userus, endometrium,

blood vessels, or related tissue, e.g. in the heart of genital tract AAY13344-403 represent secreted and transmembrane human proteins. The

Sequence 322 AA;

322 322 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: 74e-163 1657.00 100.00% 100.00% 45.98% Best Local Similarity: Percent Similarity Alignment Scores: Query Match: No.:

(1-322)US-10-079-111-2 (1-2029) x AAY13379

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CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 61

AGCTTTGAAACTTGCAGCTATGGCTTGGAGATGGATTCGTGGTCATCTCTAGGATT

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662 CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA ProGlullelleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr 141 603  $\dot{\delta}$ g

WPI; 2000-160673/14

N-PSDB; AAZ98172

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation; cardiovascular disease, anticancer; anti-inflammatory, antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antimathmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schhzophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                           AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
                                                                                                                                                                                                                                                                                                                     LysvalvalLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
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k, Hillman JL;
                                                                                TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
                                                                                               CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                                                                                                                                     GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTG
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                                                                                                                                                                                                                                                                    261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
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                         CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCCACGGAGAAAAAATTGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human signal peptide containing protein HSPP-64 SEQ ID NO:64.
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Young J, Yue H, Patterson C, Reddy R,
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AAZ38109 to AAZ98242 encode AAV87224 to AAV87357 which represent the human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have cuttonorer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antegonists of CHSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, creproductive or developmental disorders, (e.g. arteriosclerosis, creproductive or developmental disorders, (e.g. arteriosclerosis, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's asthma, confirming and partery defects, muscular dystrophy). HSPP conclete acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antieense, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping, HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists, in competitive drug screens, and for purification of HSPP from natural
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The invention relates to a novel nucleic acid encoding a PRO polypeptide. The polypeptides and polynuclectides of the invention may be useful as research tools and as therapeutics for treating enterocolitis, Zollinger-Blison syndrome, gastrointestinal ulceration, psoriasis, cancer, Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal scarring and wound healing, nerve repair, thrombosis, bone and/or cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple sclerosis, inflammatory disorders, atherosclerosis, cardiac injury, infertility, premature aging, AIDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the human PRO protein of the invention.
                                                                                                                            Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens.
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  Wood
  Pennica D,
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
Hillan K,
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  Gurney AL,
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1657.00
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  Goddard A,
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Best Local Similari
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SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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05-JAN-2000; 2000WO-US000219
                                                                                        Wood WI:
                     (GETH ) GENENTECH INC.
                                                                                                              2001-081051/09.
                                                                             Pan J,
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Best Local Similarity:
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                                         Ashkenazi AJ,
Filvaroff E, F
Godowski PJ, G
                                                                            Mather JP, F
Williams PM,
                                                                                                                                                                                                                                                                                                                                                                             Sequence 322
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                    GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
                                                                                                                                                           AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
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                                                                                                GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCCACGGCTCTG
                                                                                                                                            CTAGTGCTTGCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA
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99US-0145698P.
99US-0146222P.
99WO-US020594.
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99WO-US030911.
99WO-US030999.
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99WO-US028564
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08-SE2-1999;
13-SE2-1999;
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
29-NOV-1999;
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02-DEC-1999;
02-DEC-1999;
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20-DEC-1999;
20-DEC-1999;
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Conservative: Mismatches: Length: Matches:

Indels:

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The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis) inflammatory infertility, AIDS and diabates and retinal disorders such as retinitis phymentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and
                                                                                                                                                                                                                                                                                                                                                                                      Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
                                                                           Ą,
                                                                       ME, Goddard
Kljavin IJ,
                                 Ferrara N;
                                                                                                                                                   Tumas D;
                             Desnoyers L, Eaton DL, W, Gerber H, Gerritsen Gurney AL, Hillan KJ, F, Roy MA, Stewart TA,
Botstein D, Desnoyers ..., Fong S, Gao W, Gerber H, Grimaldi CJ, Gurney AL, F, Roy MA,
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ΡJ;

Godowski

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The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping
                                                                                                                                  Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleThrLeuValSerLysEysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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                                                         Goddard P
Wood WI;
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99WO-US021090.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development.
                 GluAsniysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
                                                                                                                                                 AGGIATGIGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
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AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polyunclectide sequences can be used in gene therapy. The polyunclectide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used as antigens in the production of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. The production of antibodies may also be used as therapeutic agents to down regulate expression and activity. The properties in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCACCCTTGTGAGAGAGAGGGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGCCAGGTGCTTCAGCCTGGTGTTCTCTCACTTCCATCTGGACCACGAGGCTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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1657.00
100.00%
100.00%
45.98%
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The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 % sequence identity to a sequence appearing as ABG95851-ABG95934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide
26-JUN-1998;
02-JUL-1998;
10-AUG-1998;
117-AUG-1998;
118-AUG-1998;
26-AUG-1998;
26-AUG-1998;
26-AUG-1998;
26-AUG-1998;
26-AUG-1998;
11-SEP-1998;
01-SEP-1998;
                                                                                                                                                     10-SEP-1998;
10-SEP-1998;
10-SEP-1998;
10-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1998;
06-OCT-1998;
08-MAR-1999;
14-MAY-1999;
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15-SEP-1999;
22-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAY-2000;
02-JUN-2000;
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                                                                                                                                                                                                                                                                  16-SEP-1998;
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                                                                                                                                      GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTG
                                                                           261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
                 AAAGTAAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
                                                                                                                                                                                  AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; transmembrane protein; antirheumatic; antiarthritic; osteopathic; sports-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG95853 standard; protein; 322 AA
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98US-0082797P
98US-008579P
98US-0085579P
98US-008759P
98US-0088021P
98US-0088030P
98US-0088030P
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98US-008882P
98US-008863P
98US-0089105P
98US-008951AP
98US-008953P
98US-0090444P
98US-0090444P
98US-0090688P
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                                                                                                                                                                                                                                                                                                                                                                    GAAGTT 1148
                                                                                                                                                                                                                                                                                                                                                                                                  GluVal 322
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15-MAY-1998
02-JUN-1998
04-JUN-1998
04-JUN-1998
10-JUN-1998
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10-JUN-1998;
10-JUN-1998;
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12-JUN-1998;
16-JUN-1998;
17-JUN-1998;
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22-JUN-1998;
24-JUN-1998;
25-JUN-1998;
25-JUN-1998;
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22-APR-1998
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110 ABG9

AAC ABG5

XXX ABG5

XXX Huma

XXX BALD1

XXX ABLD1

XXX ABLD1

XXX ABLD1

XXX ABLD1

XXX XXX BALD1

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PP 06-1

PP 06-1

PP 06-1

PP 10-1

PP 10-1

PP 11-1

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New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goddard A,
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Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US033278.
20-DEC-2000; 2000WO-US034956.
28-FEB-2011; 2011WO-US006520.
01-MARY-2001; 2011WO-US01665.
30-MAY-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US017800.
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98US-0090862P

98US-0091628P

98US-0096757P

98US-0096949P

98US-0097971P

98US-0097971P

98US-0097971P

98US-009763P

98US-009963P

98US-009963P

98US-009963P

98US-009963P

98US-009963P

98US-009963P

98US-010063P

98US-010063P

98US-010063P

98US-010093P

98US-010073P

98US-0101738P

98US-0101738P

98US-0101738P

98US-0101738P

98US-0101738P

98US-0101738P

98US-0101738P

98US-0101738P
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99WO-US020111.
99WO-US021090.
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2000WO-US004414.
2000WO-US005601.
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2000WO-US014042.
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2000WO-US023522.
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09-JUL-2001; 2001WO-US021735
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18-FEB-2000;
22-FEB-2000;
01-MAR-2000;
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17-SEP-1998;
22-SEP-1998;
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24-SEP-1998;
24-SEP-1998;
24-SEP-1998;
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Consider anothing the proteins are designated as A, B, C or D in a sample cuspected of containing an A, B, C or D plypeptide designated as A, B, C or D in a sample cuspected of containing an A, B, C or D plypeptide, by contacting the sample with a polypeptide designated as B, F, G, H or I/I polypeptide designated as B, F, G, H or I/I polypeptide designated as B, F, G, H or I/I polypeptide conjugate in the sample, where the formation of the conjugate is the presence of an A, B, C or D polypeptide, I polypeptide (C conjugate in the sample, where the formation of the conjugate is a PRO1096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5011 polypeptide, C is a PRO1096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5011 polypeptide, D is a PRO19760 polypeptide, E is a PRO5011 polypeptide, D is a PRO19760 polypeptide, D is a PRO19760 polypeptide, E is a PRO5011 polypeptide, D is a PRO19760 polypeptide, E is a PRO5011 polypeptide, D is a PRO19760 polypeptide, D is a PRO19760 polypeptide, D is a PRO19760 polypeptide and I is a PRO19760 polypeptide, E is a PRO5011 polypeptide, D is a PRO19760 polypeptide and I is a PRO19760 polypeptide designated as A, B, C or D or C is a C is a processing a polypeptide designated as A, B, C or D or C is a proposes, and as therapeutic approximate for treathing apporter artiflage defects, osteoarthritis are useful in the trapeutic apporter for proteins are useful to proposes, and as therapeutic apporter another proposes, and as therapeu for chromosome development and screening of therapeutic useful reagents, for chromosom identification, and in gene therapy. The antibody is useful as a therapyentic agent, in a diagnostic assay and for affinity purification the protein from recombinant cell culture natural sources. The present sequence represents a novel secreted or transmembrane protein of the peptide. Also included are the nucleic lacking its associated signal 

Sequence 322 AA;

322 322 0 0 0 0 Conservative: Mismatches: Length: Matches: Indels: Gaps: 3.74e-163 1657.00 100.00% 100.00% 45.98% Percent Similarity: Best Local Similarity: Query Match: DB:

US-10-079-111-2 (1-2029) x ABG95853 (1-322)

302 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 362 422 482 50 40 9 80 ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 243 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG ValGInGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 21 303 41 363 61 81 423 ð 셤 ઠે 셤 à g ò 셤 à d

1022 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT 1142 180 782 842 902 962 | GINASHINSALAA| GINASHIN | GINAS LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACATACCTGCC 161 GluphelleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuile CysvalThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal CTAGTGCTTGCTCTTCTTTTGGTGCTGCTGGTCGTCTTGGATTTTGCTATGTCAAA AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACC AAAGTAGTAAAAGGAGAGAAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA CCTACTACTACTCCTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCCACGGCTCTG GAAGTT 1148 201 221 241 963 1023 281 1083 301 1143 141 723 181 783 843 903 603 663 du g Db ò g g 8 g g d qq ò g ò ð ò à ò à ò

322 GluVal 321

ABB84832 standard; protein; 322 AA ABB84832 RESULT

(first entry) 16-MAY-2002

ABB84832;

protein sequence SEQ ID NO:32. PR0263

Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; hypertangion; arterial infarction; thrombophiebitis; wound angiogenesis; breast carcinoma; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping. 

Homo sapiens

03-JAN-2002.

20-JUN-2001; 2001WO-US019692.

23-JUN-2000; 2000US-0213637P.

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483

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AGCCCAAACCCCAAGTGTGGGAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG

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Claim 11; Fig 32; 565pp; English
                                                                                                                                                    2001WO-US006666.
2001US-00802706.
2001US-00808689.
                                                                      2000US-00665350.
2000US-0242922P.
2000US-00709238.
                                                                                                                               2001US-00767609.
2001US-00796498.
2001WO-US006520.
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2001US-00828366.
2001US-00854208.
                           2000US-0222695P.
2000US-00643657.
                                           2000WO-US023522.
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2000WO-US032678.
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2001US-00866034.
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2001WO-US017443
2001WO-US017800
             2000US-0220664P
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                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
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N-PSDB; ABL88087.
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            25-JUL-2000;
28-JUL-2000;
22-AUG-2000;
17-AUG-2000;
24-AUG-2000;
18-SEP-2000;
18-SEP-2000;
18-SEP-2000;
08-NOV-2000;
08-NOV-2000;
01-ONOV-2000;
10-NOV-2000;
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22-MAR-2001;
05-APR-2001;
10-MAY-2001;
10-MAY-2001;
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Pred. No.:
Score:
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25-MAY-2001;
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28-FEB-2001;
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Stephan JF,
                                                                                                                                                                                                                                                                       Baker KP,
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. Ferrara N, Gerber H, Gerritsen ME, Goddard A; PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, JP, Watanabe CK, Williams PM, Wood WI, Ye W;

One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.

ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABL885003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardial infarctions, thrombophebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention

322 322 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: 3.74e-163 1657.00 100.00% 100.00% 45.98% Percent Similarity: Best Local Similarity: Query Match:

GluVal

321

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RESULT

AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 1022 AAAGTAGTAAAGGAGGAGGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT 1082 140 180 902 242 302 362 422 120 662 722 782 200 842 220 240 962 260 482 100 602 40 9 80 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 21 ValGlnGlySerbeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArglle ProGluileIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluThrOPheVal GAAAATTAAAGCAGCATTCAAGAATGAAGCTGCTGGCTTTGGAGGTGTCCCCACGGCTCTG GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG <u> ATCACCCTTGTGGGCGAAAAGGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC</u> TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCCAAACTGCAACACAACACA GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 0 US-10-079-111-2 (1-2029) x ABB84832 (1-322) 1148 GAAGTT 241 1023 1143 303 363 61 423 543 121 141 201 903 963 261 281 1083 243 81 483 101 603 663 161 723 783 843 221 원 ਨੇ a ద à g ઠે 셤 ð д à 셤 à g ò g à qq à g à g ð qq ò дq ò q ò ò ò ò

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ProGlullelleThrThrLygAspProllePheAsnThrGlnThrAlaThrGlnThrThr 160
                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
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                                                                     Paoni NF;
                                                                                                                                                                                                    One hundred and eighty seven nucleic acids encoding PRO polypeptides useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           healing. The present sequence is a PRO protein of the invention
                                           cher H, Gerritsen ME, Goddard A;
Hillan KJ, Marsters SA, Pan J,
Williams PM, Wood WI, Ye W;
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                                               Gerber H,
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1657.00
100.00$
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                                                                   Godowski PJ, Gurney AL,
Stephan JF, Watanabe CK,
                                             Ferrara N,
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Best Local Similarity:
(WOOD/) WOOD W I.
                                                                                                                                                              N-PSDB; ABL95576
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                                                                                                                                                                                                  Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic.
                                                                                                                                                       Human angiogenesis related protein PRO263 SEQ ID NO: 32.
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                   protein; 322
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2001US-00802706
2001US-00816744
2001US-00816744
2001US-00828366
2001US-00854208
2001US-0086628
2001US-00866028
2001US-00866028
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2000US-0230978P
2000US-0066410
2000US-00665350
2000US-00742922P
2000WO-US030952
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2000US-0220624P.
2000US-0220664P.
2000WO-US020710.
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2000WO-US032678.
2000US-00747259.
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2001US-00796498.
2001WO-US006520.
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
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GERRITSEN M E.
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PAONI N F.
STEPHAN J F.
WATANABE C K.
                   ABB95438 standard;
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FERRARA N.
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28-JUL-2000;
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(BAKE/)
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(WILL/)
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(MARS/)
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Williams PM, Wood WI;
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22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005604.
02-MAR-2000; 2000WO-US005841.
30-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US006439.
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99WO-US030999.
2000WO-US000219.
2000WO-US003565.
                   9705-00631219-
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99WO-US021090
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2000WO-US020710.
2000WO-US023328.
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99WO-US020594.
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    24-0CT-1997;
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16-SEP-1998;
17-SEP-1998;
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GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
                                                                                                                                                                                                                                                           AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
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                                                                 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
                                                                                       CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluThrOpheVal
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Ferrara N; n ME, Goddard A; Kljavin IJ; Tumas D;

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181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
                                                                                                                                                                                                                                                                                               241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaAlaGlyLeuGlyPheCysTyrValLys
                                                                                                                                                                                                                                                                                                                                                                                               261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
                                                                                               201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                                                                                                                                                          GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGCGGTTTTGGAGGTGTCCCCACGGCTCTG
                                                                                                                                                                                                          GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
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Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
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                                                                                                                                                                  The invention relates to human PRO polypeptides (secreted or transmembrane polypeptides) and the polynucleotides encoding them. The PRO polypeptides and polynucleotides can be used in treating pathological disorders and tumours, in therapeutic treatment of cardiac insufficiency disorders and tumours, in therapeutic treatment of disorders insufficiency carecters and in therapeutic treatment of disorders insufficiency carecters and in therapeutic treatment of disorders insufficiency carecters associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal caleions, and shin diseases associated with abnormal keratinocyte differentiation (e.g., psoriases, epithelial cancers such as lung squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas). The sequences can be used as molecular markers for protein calectrophoresis purposes and can be utilised in protein-protein binding assays, biochemical screening assays, immunoassays and cell-based assays. This sequence represents a human PRO polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140
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                                             Isolated nucleic acid useful for e.g., treating pathological disorders encodes a secreted or transmembrane protein.
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                                                                                                                             English.
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Best Local Similarity:
N-PSDB; ACA59060
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2000MO-US0144042
2000MO-US015264
2000MO-US020710
2000MO-US020710
2000MO-US0203328
2000MO-US0203328
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99WO-US021547.
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22-FEB-2000;
24-FEB-2000;
02-MAR-2000;
20-MAR-2000;
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20-DEC-1999;
05-JAN-2000;
27-0CT-1997;
28-0CT-1997;
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22-MAY-2000;
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Goddard A; Kljavin IJ; Ferrara N; Tumas Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Wood WI; Williams PM,

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ProGlullelleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr

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GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla

GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC

CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal

TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT

ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuile

CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT

WPI; 2003-361832/34. N-PSDB; ACA58457.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

and transmembrane proteins (PRO polypeptides), and the polymucleotide sequences encoding them. The polymucleotide sequences are useful in molecular biology, as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polymucleotide sequences may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or their antibodies are useful in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as cancer, Allzheimer's disease or ischaemia, and in various diagnostic assays.

ABU71445-ABU71505 represent human PRO polypeptides of the invention 100 242 362 422 542 140 GICCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 302 482 120 602 662 40 9 80 secreted 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPhcThrGluAlaLysGluAla ATCACCCTTGTGAGCAAAAAGGCGAACCAGCTGAATTTCACAGAAGCTAAGGAGGCC AGCTTTGAAACTTGCAGCTATGGCTTGGAGATGGATTCGTGGTCATCTTAGGATT AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCCAAACTGCAACACAAACA TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT novel human 322 The present invention relates to the isolation of Conservative: Mismatches: Indels: Length: Matches: Gaps: US-10-079-111-2 (1-2029) x ABU71480 (1-322) Fig 74; 474pp; English. 3.74e-163 1657.00 100.00% 100.00% 45.98% Percent Similarity: Best Local Similarity: Sequence 322 AA; Alignment Scores: Pred. No.: Claim 12; 183 243 303 41 61 423 543 121 363 81 483 101 603 Query Match: No.: Score: à g ð qq à qq ò 셤 ò g  $\delta$ ద ò qq ò

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The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding PRO protein extracellular domain. Also included are a vector comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Fig 74; 484pp; English.
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1022
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               1083 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT
                                                                                                                                                                                         AAAGTAGTAAAGGAGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; transmembrane protein; PRO; gene therapy; chromosome identification; chromosome marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted/transmembrane protein PRO263.
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New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, in generating probes and in tissue typing.
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Tumas D;
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Hillan KJ, K.
Stewart TA,
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Filvaroff E, Fong S, Gao W, Gerber H,
Godowski PJ, Grimaldi JC, Gurney AL, H
Mather JP, Pan J, Paoni NF, Roy MA, S
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29-OCT-1997; 9TUS-0063435P.
29-OCT-1997; 9TUS-0063734P.
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29-OCT-1997; 9TUS-0063734P.
29-OCT-1997; 9TUS-0063738P.
29-OCT-1997; 9TUS-0064103P.
31-OCT-1997; 9TUS-0064103P.
31-OCT-1997; 9TUS-0064103P.
31-OCT-1997; 9TUS-0064103P.
31-OCT-1997; 9TUS-006610P.
31-OCT-1997; 9TUS-006610P.
31-OCT-1997; 9TUS-006610P.
31-OCT-1997; 9TUS-006610P.
31-OCT-1997; 9TUS-006610P.
31-OCT-1997; 9TUS-0066110P.
31-OCT-1999; 9TUS-0066110P.
31-OCT-1999; 9TUS-0066110P.
31-OCT-1999; 99WO-US01930.
31-OCT-1999; 99WO-US01991.
31-OCT-1999; 99WO-US01999.
31-OCT-1999; 99WO-US01999.
31-OCT-1999; 99WO-US01999.
31-OCT-1999; 99WO-US01
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the PRO nucleic acid, a host cell comprising the vector, producing a PRO polypeptide (by culturing the host cell for the expression of the PRO polypeptide (by culturing the PRO polypeptide from the cell culture), an isolated PRO polypeptide (having at least 804 sequence identity to: (C a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino acid sequence encoded by a nucleic acid molecule deposited with an ATCC number (detailed in the specification); or (C) an extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking its associated signal peptide), a chimaeric molecule comprising a PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO antibody, detecting a PRO peptide), a chimaeric molecule comprising a PRO polypeptide of fused to a cell expressing an PRO245 or PRO1868 and consistent and seample suspected of containing the polypeptide, inking a bioactive molecule to a cell expressing a PRO245 or PRO1868. Nucleic acids which encode PRO can be used to generate either transgenic animals or knock-out animals which may be used in the cacles which encode PRO can be used to generate either acids may also be used in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides and nucleic acids may also be used in diagnostic assays for PRO, and in contines are useful in diagnostic assays for PRO, and in contines. The present seminant encombinant cell culture or natural sources. The propers sources. The present sequence represents a PRO protein 

AA; Sequence 322

322 322 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: 3.74e-163 1657.00 100.00% 100.00% 45.98% Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match: Local Best

US-10-079-111-2 (1-2029) x ABU71926 (1-322)

GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 302 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 362 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGGCT 422 AGCITTGAAACTIGCAGCTATGCTTGGAGATGGATTCGTGGTCATCTTCTAGGATT 482 100 542 120 602 662 722 40 9 80 ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArg1leMetGly AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGTGTCCTGATTTGGAAGGTTCCAGTG AGCCGACAGITTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC 183 243 303 363 19 423 81 483 101 543 121 603 141 663 161 8 a ð g g qq d g a ð g à ò ò à ò à

97US-0059266P. 97US-0062125P. 97US-0062285P. 97US-0062287P. 97US-0063486P 97US-0062814P

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1022 1082 1142 902 962 300 320 diagnostic; biosensor; bioreactor; Parkinson's disease;
Alzheimer's disease; inflammation; nephritis; wound healing;
nerve repair; collateral blood vessel formation; cancer;
colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;
cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis; GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 1023 AAAGTAGTAAAAGGAGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT CysvalThrGluvalPheMetGluThrSerThrMetSerThrGluThrGluProPheVal GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTG CTAGTGCTTGCTCCTCTTTGGTGCTGCTGGTGTCTTGGATTTTTGCTATGTCAAA AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 261 ArgTyrVallysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLyrThr GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT Novel human secreted and transmembrane protein PRO263. secreted and transmembrane protein; PRO; Ŕ ABO01809 standard; protein; 322 97US-0059115P. 97US-0059117P. 97US-0059119P. 97US-0059121P. 97US-0059122P. 97US-0059184P. 97US-0059263P. 2001US-00907824 (first entry) infertility; gene therapy. 1143 GAAGIT 1148 321 Gluval 322 US2002197671-A1. sapiens 17-JUL-2001; 07-AUG-2003 17-SEP-1997 17-SEP-1997 17-SEP-1997 17-SEP-1997 17-SEP-1997 17-SEP-1997 18-SEP-1997 843 723 181 783 201 903 963 1083 ABO01809; Ношо RESULT 14 ⋧ ద ò g ò d g g Q à à ₽  $\delta$ 

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W, Gerber H, Gerritsen ME, Goddard A;
W, Hillan KJ, Kljavin IJ;
Gurney AL, Hillan KJ, Rujavin IJ;
NF, ROY MA, Stewart TA, Tumas D;
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      970S-0063045P-
970S-0063120P-
970S-0063121P-
970S-0063127P-
970S-0063127P-
970S-0063127P-
970S-0063542P-
970S-0063542P-
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970S-0063543P-
970S-0063734P-
970S-0064248P-
970S-006464P-
970S-0066344P-
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2000WO-US014042.
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20-DEC-1999;
11-FEB-2000;
24-FEB-2000;
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30-MAR-2000;
30-MAR-2000;
30-MAR-2000;
31-MAR-2000;
32-MAY-2000;
32-MAY-2000;
32-MAY-2000;
24-OCT-1997;
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27-OCT-1997;
28-OCT-1997;
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29-0CT-1997;
29-0CT-1997;
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12-NOV-1997;
17-NOV-1997;
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03-NOV-1997;
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The invention describes a new isolated nucleic acid molecule comprising
the full length coding sequence of the DNA deposited with the American
the full length coding sequence of the DNA deposited with the American
consisted the full length coding sequence of the DNA deposited with the American
with at least 80% identity to a DNA encoding a PRO polypeptide comprising
any of 61 sequences having 164-1119 amino acids fully defined in the
specification. The PRO polypeptides or polynucleotides are useful as
particularly useful for detecting or treating e.g. Parkinson's disease,
constriction and provides of particularly useful for detecting or treating e.g. Parkinson's disease,
Alzheimer's disease, inflammations, nephritis, wound healing, nerve
constriction, dammatoid or reduce risk for hemorrhage), rheumatoid
cancer), haemorrhage (or reduce risk for hemorrhage), rheumatoid
cancer), haemorrhage (or reduce risk for hemorrhage), rheumatoid
carthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
csetenosis, dermal fibrotic conditions (e.g. keloids or scarring),
cischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
cintertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
confirmed the presence of these diseases. The PRO polypeptides are useful as tryets for
therapeutic intervention in these diseases, and diagnostic determination
cof the presence of these diseases. The PRO polypeptides are also useful
as molecular weight markers, or for chromosome identification. The PRO
consumed the presence of these diseases. The PRO polypeptides are also useful
chuman cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
charapy, particularly for replacing a defective gene. This is the amino
consumed the presence of a novel human secreted and transmembrane PRO polypeptide New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO335), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia Length:
Matches:
Conservative:
Mismatches: Claim 12; Fig 74; 482pp; English. Sequence 322 AA; Alignment Scores:

3.74e-163 1657.00 100.00% 100.00% 45.98% Percent Similarity: Best Local Similarity: Query Match:

US-10-079-111-2 (1-2029) x ABO01809 (1-322)

2	1	
	183	3 AIGGCCAGGIGCTICAGCCTGGTGTTGCTTCTCCATCTGGACCACGAGGCTCCTG 242
	1	MetAlaArgCysPheSerLeuValLeuLeuThrSerIlefTrpThrThrArgLeuLeu 20
	243	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 302
	21	21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
	303	ATCACCCTTGTGAGCGAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 362
	41	41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
	363	TGTAGGCTGCGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422
	61	61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
	423	AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT 482
	81	81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVallleSerArglle 100
	483	AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTGTCTGATTTGGAAGGTTCCAGTG 542
	101	

602

543 AGCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT

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1022
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                                               722
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SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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                        GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTG
                                                                                                                                                  CTAGTGCTTGCTCCTCTTTTGGTGCTGCTGGTCTTGGATTTTTGCTATA
                                                                                                                                                                                                                GAATTTAITGECAGEGACAGTACCTACTCGGEGGCATCCCCTTACTCTACAATACCTGCC
                                                                            CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT
                                                                                                          TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
                                                                                                                                                                                                      AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACC
              201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                                                                                                                                                                                                                                               and transmembrane protein; PRO; antibody therapy; diagnostic; biosensor; bioreactor.
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Wood WI;
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Watanabe
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C, Gurney 1
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pharmaceutical;
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The invention describes an antibody that specifically binds to a PRO polypeptide having a fully defined amino acid sequence given in the specification. The antibody is useful in identifying PRO polypeptides useful for various industrial applications, including pharmaceuticals, diagnostics, biosensors and bioreactors. The antibody is also used for affinity purification of PRO polypeptides from recombinant cell culture or natural sources. The antibody, PRO polypeptide, or its agonists or antagonists, may be used for preparing a medicament for diagnosing or treating a condition responsive to the antibody, PRO polypeptide, or its agonists or antagonists. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
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New antibody useful for identifying PRO polypeptides, for affinity purification of PRO polypeptides, and for preparing a medicament for diagnosing or treating conditions responsive to the antibody or PRO
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963 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACC 1022
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                                                                                                                                           261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMet1leGluThr 280
                                                                                                                                                                                            201 CysvalThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
                                        903 CTAGTGCTTGCTCTCTTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 962
                                                                                          241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
                           GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTG 902
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION:
CURRENT PAIGN WINDER: US/10/276,774
CURRENT FAILING DATE: 2002-11-18
PRIOR PRILICATION NUMBER: US/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 2349
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Sequence 2349, Application US/10276774
Publication No. US20040053245A1
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Maximum Match 100%
Listing first 45 summaries
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Minimum DB Maximum DB

Searched:

Alignment Scores:

Score

Result No.

QY         1077 ABAACTGATAAAAACCCGGAAGACTCCAAGGCAAAACTACCGTGGATGCCTG         1136           Db         321 LysThlaspLysAsnProdluGluSerLysSerProSerLysThrThrMetArgCysLeu         340           QY         1137 GAAGCTGAAGTT         1148           Db         341 GluAlaGluVal         344	NESULI 2	APPLICANT: Genentech, Inc. ; APPLICANT: Ashkenazi, Avi ; APPLICANT: Bestein, David		; APFILCANT: FOUR ALCHAUMAIN; APPILCANT: Gao, Wel-Qlang; APPILCANT: Gerber, Hanspeter; APPILCANT: Geritleen, Mary E.		Kljavin, Ivar J. Mather, Jennie P. Pan, James	; APPLICANT: Padoni, Nicholas F. ; APPLICANT: Roy, Margaret Ann ; APPLICANT: Stewart, Timothy A. ; APPLICANT: Tumas, Daniel ; APPLICANT: Tumes, Daniel	APPLICANT: Wood, William, I	; FILE KEREKINCE: 104809: 120 ; CURRENT APPLICATION NUMBER: US/09/909,320 ; CURRENT FILING DATE: 2002-01-04 ; PRIOR APPLICATION NUMBER: PCT/US00/04414	FRIOR APPLICATION NUMBER: US 60/143,048 ; PRIOR FILING DATE: 1999-07-07 ; PRIOR FILING NUMBER: US 60/145,698	FRIOR APPLICATION UNRBER: US 60/146,222 ; PRIOR FILING DATE: 1999-07-28 ; PRIOR FILING DATE: 1999-07-28 ; PRIOR PELING NUMBER: PCT/US99/20594	FRIOR APPLICATION NUMBER: PCT/US99/20944 ; PRIOR FILING DATE: 1999-09-13 ; PRIOR FILING NUMBER: PCT/US99/21090 ; PRIOR PILING NUMBER: PCT/US99/21090	FRIOR APPLICATION UNRBER: PCT/US99/21547 ; PRIOR FILING DATE: 1999-09-15 ; PRIOR FILING DATE: 1999-09-15 ; PRIOR FILING NUMBER: PCT/US99/23089	# PRIOR APPLICATION NUMBER: PCT/US99/28214  # PRIOR FILING DATE: 1999-11-29  # PRIOR PILING DATE: 1999-11-29  # PRIOR PILING NUMBER: PCT/US99/28313  # PRIOR PILING NUMBER: PCT/US99/28313	PRIOR APPLICATION NUMBER: PCT/US99/28564   PRIOR FILING DATE: 1999-12-02   PRIOR PPLICATION NUMBER: PCT/US99/28565	FRIOR APPLICATION NUMBER: PCT/US99/30095   PRIOR FILING DATE: 1999-12-16   PRIOR FILING DATE: 1999-12-16   PRIOR APPLICATION NUMBER: PCT/US99/30911   PRIOR FILING DATE: 1999-12-20
Pred. No.: 5.41e-159 Length: 344 Scorer: 172.00 Matches: 343 Percent Similarity: 100.00\$ Conservative: 1 Best Local Similarity: 99.71\$ Mismatches: 0 Query Match: 12 Gaps: 0 US-10-079-111-2 (1-2029) x US-10-276-774-2349 (1-344)	Qy         117 GCATCTGCTCTCATATCACCAGTGGCCATCTGAGGTTTCCCTGGCTCTGAAGGGCTA         176           Db         1 AlaSerAlaSerHisileThrSerGlyHiBLeuArgCysPheProGlySerGluGlyVal         20	Qy 177 GGCACGATGGCCTCAGCCTGGTGTTCTCACTTCCATCTGGACCACGAGG 236	Oy 237 CTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGGCTTTCCATCCA	Qy 297 ATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAG 356	OY 357 GAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTG 416	QY         417 AAAGCTATGAACTTTGAAACTTGCAGCTATGGGTTGGAATGGATTCGTGGTCATCTCT         476           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 477 AGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGGTGGGGTGTCCTGATTTGGAAGGTT 536	Qy 537 CCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCG 596	Qy 597 TGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACAA 656	Oy 657 ACAACAGAATITATIGICAGTGACAGTACCTACTCGGTGGGATCCCCTTACTCTACAATA 716	Qy 717 CCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAA 776	Qy 777 TIGAHTHGTGTCACAGAAGTHTTTAHGGAAACTAGCACCATGTCTACAGAAACTGAACCA 836	Qy 837 TTTGTTGAAAATAAAGCAGTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACG 896	Qy         897 GCTCTGCTAGTGCTTGCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTAT         956           Db         261 AlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaAlaGlyLeuGlyPheCysTyr         280	Qy 957 GTCAAAAGGTATGTGAAGGCCTTCCCTTTACAAACAAGAATCAGCAGAAGGAAATGATC 1016	Oy 1017 GAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAG 1076

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AAAGTAGTAAAGGAGGAGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT 1082
                                                                                                                        301 AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
     241 LeuValLeuAlaLeuLeuPheFheGlyAlaAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
                                                                                                                                                                     GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT
                                                          APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT PEPLICATION NUMBER: US/09/909,088B
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US/US00/04414
PRIOR FILING DATE: 1090-02-22
PRIOR PELING DATE: 1099-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: US/US99/2054
PRIOR PELING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
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Gao, Wal-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J
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Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Botstein, David
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Eaton, Dan L.
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GENERAL INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-112-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 201
LENGTH: 322
                                                                                                                                                           ; OTHER INFORMATION: Synthetic protein US-09-909-320-201
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1657.00
100.00%
100.00%
45.98%
                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
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Query Match:
DB:
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Pred. No.:
Score:
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                                              201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                                                                                                                            843 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
                                                                                                                                                              221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu
                                                                                                                                                                                                                                                                                                                                                                              261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
                 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/905,291A

CURRENT FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: US/09/905,291A

PRIOR FILING DATE: 2000-02-2

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-06

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

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PRIOR FILING DATE: 1999-07-28

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US-09-905-291A-201
Sequence 201, Application US/09905291A
Patent No. US20020160374A1
GENERAL INFORMATION:
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Gerber, Hangpeter
Gerritsen, Mary E.
Goddard, A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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PRIOR APPLICATION NUMBER: PCT/US99/28113
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
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                                                                                  161 GluPheileValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla
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                                                                                                                              CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT
                                                                                                                                                                                                          TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
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CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
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Publication No. US20020192659A1
GENERAL INFORMATION:
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-00-15

PRIOR PLING DATE: 1999-10-05

PRIOR PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-11-29

PRIOR PRIOR DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-20

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-03

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                                                                     261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
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Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, Davi
APPLICANT: Desnoyers, Luc
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PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
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PRIOR PELING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21847
PRIOR PILING DATE: 1999-10-05
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; ORGANISM: Homo Sapien
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; Sequence 201, Application US/09907841; Publication No. US20020198366A1; GENERAL INFORMATION:
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Botsnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane
FILE REPERNET: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US/065,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-22
PRIOR PLICATION NUMBER: US 60/145,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-28
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PRIOR PLING DATE: 1999-09-15
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PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/280-19
PRIOR PLING DATE: 1999-09-15
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PRIOR PLING DATE: 1999-11-20
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PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/286-6
PRIOR PLING DATE: 1999-12-02
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SEQ ID NO 201
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: Homo
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US-09-907-824-201
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                                                          ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
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CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
                                                                                                                                                 AGCCCAAACCCCCAAGTGTGGGGAAAAATGGGGTGTGTCCTGATTTGGAAGGTTCCAGTG
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                                                                                                                           201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr
       123 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTTAGGATT
                                                                                                AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
                                                                                                                                                                                          543 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT
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Geritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
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Publication No. US20030003530A1
GENERAL INFORMATION:
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Filvaroff, Ellen
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Botstein, David
Desnoyers, Luc
Eaton, Dan L
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, I.
APPLICANT: Wold, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US 09/907,841
CURRENT FILING DATE: 2000-11-20
FRICH FILING DATE: 1090-10-22
FRICH APPLICATION NUMBER: US 60/143,048
FRICH FILING DATE: 1999-07-06
FRICH APPLICATION NUMBER: US 60/145,698
FRICH RILING DATE: 1999-09-08
FRICH RILING DATE: 1999-09-08
FRICH RILING DATE: 1999-09-08
FRICH FILING DATE: 1999-09-08
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FRICH FILING DATE: 1999-09-08
FRICH FILING DATE: 1999-09-18
FRICH RILING DATE: 1999-09-15
FRICH FILING DATE: 1999-09-15
FRICH RILING DATE: 1999-00-15
FRICH RILING DATE: 1999-00-15
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FRICH RILING DATE: 1999-10-05
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Mismatches:
Indels:
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Grimaldi, Christopher
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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                     Gurney, Austin L.
Hillan, Kenneth, J
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                                                                   Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Best Local Similarity:
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Pred. No.:
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LENGTH: 322
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              41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla
                                                                                                                                363 IGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCTTGAAAGCT
                                                                                                                                                     61 CysArgheuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
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                                                                 303 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAAGGAGGCC
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US-09-906-742-201
i Sequence 201, Application US/09906742
j Publication No. US20030023054A1
i GENERAL INFORMATION:
i APPLICANT: Genettech, Inc.
i APPLICANT: Bottein, David
i APPLICANT: Bottein, David
i APPLICANT: Beston, David
i APPLICANT: Eaton, Dan L.
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APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Twar J.
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APPLICANT: Rainie Pan, James
APPLICANT: Rainie Pan, James
APPLICANT: Rainie Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Stowner, Timothy A.
APPLICANT: Stowner, Timothy A.
APPLICANT: Mondal Millani, P. Mickey
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APPLICANT: Mondal Millani, P. Mickey
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Pred. No.:
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APPLICANT: Pan, Januara P.
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APPLICANT: Pan, Januara P.
APPLICANT: Roy, Magazet Ann
APPLICANT: Roy, Magazet Ann
APPLICANT: Roy, Magazet Ann
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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PRIOR PLILING DATE: 1999-0-22
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PRIOR PLILING DATE: 1999-0-34
PRIOR PLILING DATE: 1999-1-120
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Matches:
Conservative:
Mismatches:
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                                                                                                                                            Godowski, Paul J.
Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
  Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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1657.00
100.00%
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                                                                                     Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                   Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                          Goddard, A.
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; ORGANISM: Homo Sapien
US-09-906-742-201
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CURRENT APPLICATION NUMBER: US/09/906,838

CURRENT APPLICATION NUMBER: O9/66,350

FRIOR FILING DATE: 2000-02-22

FRIOR APPLICATION NUMBER: POT/05/918

FRIOR APPLICATION NUMBER: US 60/145,698

FRIOR APPLICATION NUMBER: US 60/145,698

FRIOR APPLICATION NUMBER: US 60/146,222

FRIOR APPLICATION NUMBER: POT/US99/20594

FRIOR FILING DATE: 1999-00-38

FRIOR FILING DATE: 1999-00-38

FRIOR FILING DATE: 1999-00-48

FRIOR PELING DATE: 1999-00-48

FRIOR FILING DATE: 1999-00-41

FRIOR PELING DATE: 1999-00-41

FRIOR FILING DATE: 1999-10-12

FRIOR APPLICATION NUMBER: POT/US99/2814

FRIOR APPLICATION NUMBER: POT/US99/2814

FRIOR APPLICATION NUMBER: POT/US99/2814

FRIOR APPLICATION NUMBER: POT/US99/2816

FRIOR FILING DATE: 1999-11-20

FRIOR FILING DATE: 1999-12-02

FRIOR FILING DATE: 1999-12-03

FRIOR FILING DATE: 2000-01-05

FRIOR FILING DATE: 2000-01-05
RESULT 10
US-09-906-838-201
US-09-906-838-201
Sequence 201, Application US/09906838
Sequence 201, Application US/09906838
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.;
APPLICANT: Ashkenazi, Avi;
APPLICANT: Botstein, David
APPLICANT: Eacon, Dan L.
APPLICANT: Ferrara, Napoleone
                                                                                                                                                                                                                                                                                 Gerber, Hanspeter
Gerritsen, Mary B.
Geddard, A.
Goddwaki, Paul J.
Grimaldi, Christopher J.
Grimaldi, Christopher J.
Kliavin, Ivar J.
Mather, Jennes P.
Pan, James
Paoni, Nicholas F.
                                                                                                                                                                                                         Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
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                                                                                                Length:
Matches:
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Mismatches:
Indels:
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45.98%
                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo S
US-09-906-838-201
                                                                                    Alignment Scores:
Pred. No.:
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121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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Mismatches:
Indels:
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Matches:
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PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR PLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-907-613-201
                                                                                                                                                                                                                                                                                                               4.44e-148
1657.00
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                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial sequence
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LENGTH: 322
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APPLICANT: Turnas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFRENCE: 10466-14
CURRENT FILING DATE: 2001-07-17
FRICA PAPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1995-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR FILING DATE: 1995-07-26
PRIOR PLING DATE: 1995-09-13
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PRIOR APPLICATION NUMBER: PCT/US99/2109
PRIOR PLING DATE: 1995-09-13
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PRIOR PLING DATE: 1995-09-15
PRIOR PLING DATE: 1995-11-29
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                                                                  301 AsplysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
  281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
                                         1083 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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1 Sequence 201, Arr

2 Publication No. US200...

3 APPLICANT: Genentech, Inc.

- "PLICANT: Ashkenazi, Avi

"PLICANT: Ashkenazi, Avi
"": Botstein, David
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Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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1 MetAlaArgCysPheSerLeuValLeuLeuLeuChrSerIleTrpThrThrArgLeuLeu
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
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PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
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PRIOR PLING DATE: 2000-01-05
PRIOR PLING DATE: 300-01-05
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Best Local Similarity:
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                         241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys
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                                                                                                                                                                                         Transmembrane Polypeptides and Nucleic
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wolliams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane P.
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/907,942
CURRENT APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PRILING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-15
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PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/213089
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-09-15
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Publication No. US20030027146A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
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Stewart, Timothy A.
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Gerritsen, Mary E.
Goddard, A.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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TYPE: PRT
ORGANISM: Homo Sapien
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Best Local Similarity:
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US-09-904-859-201
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ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
FILE REFERENCE: 10466-14
CURRENT PREPAIRON NUMBER: US/09/904,859
CURRENT PILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1090-07-27
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
                                                                                        GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG
                                                                                                                                                  CTAGTGCTTGCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Williams, P. Mickey
Wood, William, I.
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Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Iuc
APPLICANT: Eaton, Dan i.
APPLICANT: Perrara, Napoleon
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Paoni, Nic
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Publication No. US20
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
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PRIOR PILING DATE: 1999-10-05
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        CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-2
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PRIOR PLING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
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PRIOR PLING DATE: 1999-09-13
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ORGANISM: Artificial sequence
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
ProGlullelleThrThrLygAspProllePheAsnThrGlnThrAlaThrGlnThrThr
                                                                             GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC
                                                                                                                                                            CCTACTACTACTCCTCCTCCTCCTCCTCCTTCTATTCCACGGAGAAAAATTGATT
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; Publication No. US2003003661A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Betetein, David
; APPLICANT: Betatein, David
; APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Eaton, Dan L.
Ferrara, Napoleone
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Goddard, A.
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Gao, Wei-Qiang
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APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Wood, William:
ITILE OF INVENTUON: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT APPLICANT: Wood, William:
FILE REFERENCE: 10466-118
CURRENT APPLICATION NUMBER: US/09/904,820
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: PET/USO/0414
PRIOR APPLICATION NUMBER: PET/USO/0414
PRIOR PELING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PET/USO/04414
PRIOR PELING DATE: 1999-07-28
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Conservative:
Mismatches:
Indels:
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                         Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Best Local Similarity:
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                                                                                                                                                           SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
                                                                                                                                                                                                                                                     141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr
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                                                                    543 AGCCGACAGITIGCAGCCIATIGITACAACICATCIGATACTIGGACIAACTCGIGCAIT
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                                           483 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG
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Gerritsen, Mary B.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Publication No. US20030036094A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Behtenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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US-09-904-820-201
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362 60	422 80	482	542	602	662 160	722	782	842	902	962	1022	1082	1142		
ATCACCCTTGTGAGCAAAAAGGCGAACCAGCGGCTGAATTTCACAGAAGCTAAGGAGGCC 	TGTAGGCTIGCTGGGACTTAGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 		AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT	CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACACA	GAAITTATIGICAGIGACAGTACCIACIACIGGGAICCCCTTACICTGCAATACCIGCC		TGTGTCACAGAAGTTTTTATGGAAACTAGGACCATGTCTACAGAAACTGAACGATTTGTT 	GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	CTAGTGCTTGCTCTCTTTTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA	AGGTATGTGAAGGCCTTCCCTTTACAACAAGAATCAGCAGAAGGAAATGATCGAAACC	AAAGTAGTAAAGGAGAGAGAGCCAATGATGACAACCCTAATGAGGAATCAAAGAAAACT	GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT	GAAGTT 1148         GluVal 322	
303	363	423	483	543	603	663	723	783	843	903	963	1023	1083	1143	
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Search completed: September 13, 2004, 10:32:08 Job time : 213.5 secs

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September 13, 2004, 10:05:16; Search time 74.5 Seconds (without alignments) 5239.533 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                  using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                           283366 segs, 96191526 residues
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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3604
                                                                  OM nucleic - protein search,
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Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/Cqg12\_1/USPTO\_spool\_p/US1009111/runat\_13092004\_102127\_1835/app\_query.fasta\_1.2183
-Q=/Cqg12\_1/USPTO\_spool\_p/US1009111/runat\_13092004\_102127\_1835/app\_query.fasta\_1.2183
-DB=PIR\_78 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPEXT=0
-UNITS=EDIAS -START=1 -END=-1 -MATRIX-EDI-OSMMG2 -TRANS=Duman40.cdi -LIST=45
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTRW=pct -NORM=ext -HEAPSTE=500 -MINLEN=0 -WAXLEN=2000000000
-USRE-US10079111\_@CGN 1\_1104\_grunat\_1309204\_102127\_1835 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG
-NORM-EXT -NEG SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

pirl:\* pir2:\* pir3:\* pir4:\* PIR\_78:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Cocitairosed		CD44 homolog membr	cell adhesion mole	lymphocyte adhesio	CD44 membrane glyc	T-cell surface giv	lymphocyte homing	cell-surface glyco	epican - human	cell adhesion mole	CD44E protein, epi	CD44 antiqen precu	lymphocyte homing	CD44R5 - human	lymphocyte surface
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EC.		7	~	~	~1	~	7	~	7	~	~	7	~	~	7
* Query Match Length DB		363	503	362	365	362	742	366	669	361	493	351	426	395	359
% Query Match		6.4	6.3	6.2	6.2	9	6.0	5.8	5.8	5.7	5.7	5.6	5.6	5.5	5.2
Score	1 1	229.5	228.5	222.5	222.5	217.5	215.5	208.5	208	205	204	202.5	202.5	198	186
Result No.	1	-	71	m	4	2	9	7	8	6	10	11	12	13	14

chondroitin sulfat	aggrecan precursor hyaluronate-bindin	hypothetical prote	tumor necrosis fac	proteoglycan core	aggrecan - bovine	aggrecan precursor	TSG-6 homolog PS4	proteoglycan core	aggrecan precursor		brevican precursor	brevican precursor	neurocan precursor	versican precursor	brain link protein	hypothetical prote	aggrecan - pig (fr	hypothetical prote	versican precursor	versican precursor	chitinase (EC 3.2.	hypothetical prote	glycoprotein I pre	neurocan - mouse	dihydrolipoamide a	LDL receptor 2 pre	3	proteoglycan link	proteoglycan link
	1 150421 2 A41735	2 T42681	2 JC6506											1 A55535		2 T21700		2 T33922	2 T14274			2 T29818			2 873773	1 QRXLL2	1 A60979	1 LKHU	1 LKCH
3562	277	1069	275	1340	2327	2415	276	2124	2132	912	883	883	1257	2397	340	846	370	1360	1643	3381	099	645	390	1268	402	606	2409	354	355
4.4	4.0	4.0	4.0	4.0	•	٠	3.8	•	•	3.6	3.6	3.6	3.5	3.4	3.2	3.2	3.2	3.2	3.5	3.2	3.2	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.0
152.5	145	145	144	143.5	143	138.5	137	136.5	132.5	131.5	130.5	130.5	126	122	117	116	115	115	115	115	114.5	113	112	112	111.5	111.5	111	110	109.5
15	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31			34	35		37	38			41	42	43	44	45

## ALIGNMENTS

RESULT 1 A37009

CD44 homolog membrane glycoprotein precursor - mouse C;Species: Mus musculus (house mouse)	C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 21-Jul-200 C:Acression: A37009	X,Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, B.C.; G. J. Immunol. 143, 3390-3395, 1989	A; Title: Molecular cloning and expression of Pgp-1. The mouse homolog of t A; Reference number: A37009; MUID:90038499; PMID:2681416	A,Accession: A37009 A,Status: preliminary	A;Molecule type: mRNA A;Residues: 1-363 <zho></zho>	A;Cross-references: GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333 C;Superfamily: human cell adhesion protein CD44
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 21-Jul-200 C;Accession: A37009 R;Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, E.C.; G R;Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, E.C.; G A;Title: Molecular cloning and expression of Pgp-1. The mouse homolog of the A;Reference number: A37009; MUID:90038499; PMID:2681416 A;Accession: A37009 A;Accession: A37009 A;Accession: A37009 A;Accession: A37009 A;Accession: A37009 C;Superfaminary A;Molecule type: mRNA A;Residues: 1-363 <zho> C;Superfamily: human cell adhesion protein CD44</zho>	Rizhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, E.C.; G. J. Immunol. 143, 3390-3395, 1989 J. Immunol. 143, 3390-3395, 1989 J. Immunol. 143, 3390-3395, 1989 J. Title: Molecular cloning and expression of Pgp-1. The mouse homolog of the Reference number: A37009 MUID:90038499; PMID:2681416 A.Accession: A37009 A.Status: preliminary A.Molecule type: mRNA A.Residues: 1-363 <zho> A.Cross-references: GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333 C.Superfamily: human cell adhesion protein CD44</zho>	A;Title: Molecular cloning and expression of Pgp-1. The mouse homolog of t A;Reference number: A37009; MUID:90038499; PMID:2681416 A;Accession: A37009 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-363 <zho> A;Cross-references: GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333 C;Superfamily: human cell adhesion protein CD44</zho>	A, Accession: A37009 A, Status: preliminary A, Molecule type: mRNA A, Residues: 1-363 < ZHO> A, Cross-references: GS: NID: G200332; PIDN: AAA39922.1; PID: G200333 C, Superfamily: human ceil adhesion protein CD44	A;Molecule type: mRNA A;Residues: 1-363 <zho> A;Cross-references: GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333 C;Superfamily: human cell adhesion protein CD44</zho>	A;Cross-references: GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333 C;Superfamily: human cell adhesion protein CD44	
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 21-Jul-200 C;Date: 31-Jan-1992 #text_change 21-Jul-200 C;Accession: A37009 R;Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, E.C.; G J. Immunol. 143, 3390-3395, 1989 A;Title: Molecular cloning and expression of Pgp-1. The mouse homolog of tA;Reference number. A37009; MUID:90038499; PMID:2681416 A;Accession: A37009 A;Accession: A37009 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-363 cZHO> A;Residues: 1-363 cZHO> A;Coss.references: GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333 C;Superfamily: human cell adhesion protein membrane protein	Rizhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, E.C.; G. J. Immunol. 143, 3390-3395, 1989 J. Immunol. 144, 3390-3395, 1989 J. Title: Molecular cloning acxpression of Pgp-1. The mouse homolog of the Arcession A37009 MUID:90038499; PMID:2681416 A.Accession. A37009 A.Status: preliminary A.Molecule type: mRNA A.Kesidues: J-363 xHO A.Kesidues: J-363 xHO A.Cross-references: GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333 C.Superfamily: human cell adhesion protein cD44 C.Keywords: cell adhesion; glycoprotein; membrane protein	A;Title: Molecular cloning and expression of Pgp-1. The mouse homolog of t A;Reference number: A37009; MUID:90038499; PMID:2681416 A;Accession: A37009 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-363 <zho> A;Cross-references: GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333 C;Superfamily: human cell adhesion protein CD44 C;Keywords: cell adhesion; glycoprotein; membrane protein</zho>	A;Accession: A37009 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-363 <zho> A;Cross-references: GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333 C;Superfamily: human cell adhesion protein CD44 C;Keywords: cell adhesion; glycoprotein; membrane protein</zho>	A,Molecule type: mRNA A,Residues: 1-363 × ZHO-> A,Residues: 1-363 × ZHO-> A,Cross-references: GB.M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333 C,Superfamily: human cell adhesion protein CD44 C;Keywords: cell adhesion; glycoprotein; membrane protein	A;Cross-references: GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333 C;Superfamily: human cell adhesion protein CD44 C;Keywords: cell adhesion; glycoprotein; membrane protein	C, Keywords: cell adhesion; glycoprotein; membrane protein

log of the human H-CAM E.C.; Goeddel, D.V.

-Jul-2000

363 89 57 148 63 Length:
Matches:
Conservative:
Mismatches:
Indels: 6.93e-12 229.50 40.90% 24.93% 6.37% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB: Score:

US-10-079-111-2 (1-2029) x A37009 (1-363)

275	25	335	45	395
225 TGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCC 275		276 ATCCAGGIGICATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGCAG 335	26 LeudsnValThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSer 45	336 CTGAATTTGACAGAAGCTAAAGAGGCTGTAGGCTGGGGACTAAGTTTGGCCGGCAAG 395
22		27	7	33
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285 TCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTC 344
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30 ThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSerIleSerArg
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                  A Molecule type: mRNÅ
A;Residues: 1-503 <GUE>
A;Residues: 1-503 <GUE>
A;Residues: 1-503 <GUE>
A;Residues: 1-503 ,40E>
A;Residues: 1-223,386-503 <GUE>
A;Residues: 1-223,386-503 <GUE>
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Matches:
Conservative:
Mismatches:
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36.19%
24.51%
                                                                                                                                                       A; Cross-references: GB: M61875
C; Keywords: cell adhesion
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Best Local Similarity:
  A;Status: preliminary
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1992 #text_change 05-Nov-1999
C;Accession: B38745; A38745
R;Guenthert, U.; Hofmann, M.; Rudy, W.; Reber, S.; Zoeller, M.; Haubmann, I.; Matzku, Cell 65, 13-24, 1991
A;Title: A new variant of glycoprotein CD44 confers metastatic potential to rat carcin A;Reference number: A38745; MUID:91191552; PMID:1707342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        984 TTTACAAACAAGAATCAGCAGAAGGAAATGATC-----GAAACCAAAGTAGTAAAG 1034
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294 ArgArgCysGlyGlnLysLysLysLeuVallleAsnGlyGlyAsnGlyThrValGlu 313
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                                                                        66 AspGlnMetLysLeuAlaLeuSerLysGlyPheGluThrCysArgTyrGlyPheIle---
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                                                                                                                                                                                                                                                                                                            SerAlaProProGluGluAspCys------ThrSerValThrAspLeuPro
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46 IleSerArgThrGluAlaAlaAspLeuCysGlnAlaPheAsnSerThrLeuProThrMet
                                                                                                                 456 GATGGATTCGTGGTCATCTCTAGGATTAGCCCCAAACCCCCAAGTGTGGGAAAAATGGGGTG
                                                                                                                                                                                                                                                                                                                                                   AACACTCAAACTGCAACACAACAACAACAGAATTTATTGTCAGTGACAGTACC---TACTCG
                                                                                                                                                                                                                                                                                                                                                                                     140 AsnSerPheAspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSer
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                                                                                                                                                                                             516 GGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ACTACTCCTGCT----CCAGCTTCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              816 ATGTCTACA---GAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAG------
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881

predicted <MAT>

#status

0/Domain: extracellular #status predicted <EXT>

2/Product: lymphocyte adhesion receptor

ò	933 GCAGCTGGTCTTGCAITTTGCTAIGTCAAAAGGTATGTGAAGGCCTTCCTTTT	986	F;21-362
qa	 264 AspArgAsnSerThrSerAlaHisGlyGluAsnTrpThrGlnGluProGlnProProPhe	283	F;21-270 F;271-29
ζ	987 ACAAACAAGAATCAGCAGAAGGAAATGATC	1016	F;291-36 F;25,57,
Db	 	303	F;296/Bi
δλ	1017 GAAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAG	1076	Alignmen Pred. No
οg	304 AspProAsnSerThrThrGluGluAlaAlaThrGlnLysGluLysTrpPheGluAsnGlu	323	Score: Percent
ò	1077 AAAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACC	1124	Best Loc Query Ma
qa	324 TrpGlnGlyLysAsnProProThrProSerGluAspSerHisValThrGluGlyThrThr	343	DB:
ζŏ	1125 GTGCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACA	1175	/0-0T-80
Db	 	363	Ši iš
ζŏ	1176 CCTGAGGCTGGTTTCTTCATGCTCCTTACCCTGCCCAGCTGGGGAAAATCAAAAGGGCC	1235	qq
QQ		379	ð
Ολ	1236 AAAGAACCAAAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCA 129	1295	QQ
qa	380 HisGlnThrGluSerLysGlyHisSerSerGlyAsn	391	ð í
Ολ	1296 TIGGACTAIGGAGIGCACCAAAGAGAAIGCCCTICTCCITAITGIAACCCIGIC	1349	g (
qa	392 GlnAspSerGlyValThrThrThrSerGlyProAlaArgArgProGlnIleProGlu	410	Āō i
λō	CTA	1409	Dp
qq		428	ð í
ò	1410 ATAATATCCCACTGGGAGAAAGGGGTTTTGCAAAGTGCAAGGACCTAAAACATCTCATCA	1469	QQ
ДD	:::        ::: 429IleAlaValAsnSerArgArgArgCysGlyGlnLysLysLeuVal-	444	ò
λ̈	1470 GTATCCAGTGGTAAAAAGGCC	1490	qa
Db		464	Š
δλ	1491 TCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCT	1547	Dp
Dþ		484	ði i
δλ	1548 TICTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA 1583		DP
qq	485 PheMetThrAlaAspGluThrArgAsnLeuGlnSer 496		ð í
RESULT 3	JLT 3		qq

ò g B &  $\delta$ 셤 \triangle \trian Š Typinglance automotory procursor.

Cypecies: Papio sp. (baboon)
Cybate: 18-Apr-1989 #sequence\_revision 18-Apr-1989 #text\_change 21-Jul-2000
Cyaccession: A33935; A30901
R;Idcarda, R.L.; Carter, W.G.; Nottenburg, C.; Wayner, E.A.; Gallatin, W.M.; St. John, T Proc. Natl. Acad. Sci. U.S.A. 86, 4659-4663, 1989
A;Title: Isolation and DNA sequence of a cDNA clone encoding a lymphocyte adhesion recep A;Reference number: A33935; MUD:89282830; PMID:2471974
A;Accession: A33935
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <1D2
A;Cross-references: GB:M22452; NID:g176576; PID:g176577
C;Comment: This protein was isolated from the herpes papio induced B cell lymphoma.
C;Genetics:
A;Gene: CD4; ECMRIII; Hermes-1 antigen
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cytoskeleton; extracellular matrix; glycoprotein; lipoprotein; surface antig
F;1-20/Domain: signal sequence #status predicted <SIG> lymphocyte adhesion receptor precursor - baboon

250

g

090/Domain: transmembrane #status predicted <TMM> 662/Domain: intracellular #status predicted <CTMT> 7,100,110,120,256/Binding site: carbohydrate (Asn) (covalent) #status predicted sinding site: palmitate (Cys) (covalent) #status predicted 479 359 539 91 IleHisProAsnSerlleCysAlaAlaAsnAsnThrGlyValTyrileLeuThrSerAsn 110 599 629 144 716 728 210 860 360 GCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAA 419 111 Thrser---GlnTyrAspThrTyrCysPheAsnAlaSerAlaProProGlyGluAspCys 129 145 IleThrIleValAsnArgAspGlyThrArgTyrValLysLysGlyGluTyrArgThrAsn 164 184 204 800 229 881 249 51 71 90 GGGATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAG 420 GCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTTAGG 52 LeuCysLysAlaPheAsnSerThrLeuProThrMetAlaGlnMetGluLysAlaLeuSer ATTAGCCCAAACCCCAAGTGTGGGAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCA -----ThrSerValThrAspLeuProAsnAlaPheAspGlyProIleThr ||| | ProGluAspIleAsnProSerSerProThrAspAspAspValSerSerGlySerSer 741 GCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTCACAGAAGTTTTT 600 ATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAAACTGCAACACAAACA 660 ACAGAATTTATTGTCAGTGACAGTACC---TACTCGGTGGCATCCCCTTACTACAATA ---ACTACTCCTCT ATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTC ---ProTrpIleThrAspSerThrAspArgThrProAlaThrArgAspGlnGlyAlaPhe -- GTCCCCACG GIGAGCCGACAGTITGCAGCCTATIGITACAACTCATCTGATACTIGGACTAACTCGTGC ---AATGAAGCTGCTGGTTT------362 92 43 127 127 16 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: ----GCCCCTACT-----79-111-2 (1-2029) x A30901 (1-362) 205 IleProAspGluAspGly----2.89e-11 222.50 37.40% 25.48% 6.17% AAG-----Similarity: CCT Similarity: Scores: 300 32 480 540 130 717 165 185 801 729 211 882

956 Qy 450 GTTGG	287 Db 86	1016 Qy 510 GGGTGGGTGTCTGATTTGGAAGGTTCCAGTGACGCGACAGTTTGCAGCCTATTGTTAC 313 Db 105 HisThxGlyValTyrIleLeuValThxSerAsnThxSerHisTyrAspThxTyrCysPhe	1267 OY STO AACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCC	2y 630 ATATTCAACACTCAAACTGCAACACAAACAACAATTTATTGT 1::	Qy 687 TACTCGGTGGCATCCCCTTACTCTACA	714	Db 180 AspAspAssPValSerSerGlySerThrIleGluLysSerThrProGluSerTyrIleLeu  Qy 753ACTTCTATTCCACGGAGAAAAAATTGATTTGTCACAGAAGTTTTTATGGAAACT        :::        Db 200 HisThrTyrLeuProThrGluGlnProThrGlyAspGlnAspAspSerPhePheIleArg	om the primate Qy 810 AGCACCATGTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAAG	Qy 864 - Db 240 V	<pre>; August, J.T. Qy 888</pre>	Qy 918 CTCTTCTTTGGTGCAGCTGGACTTTGGATTTTGCTATGTCAAAAGGTATGTAAAGGCC	Qy 978 TTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAAGTA	1029	П	333	RESULT 5 3569 A35616 T-cell surface glycoprotein CD44 - hamster C;Species: Cricetinae gen. sp. (hamster)	C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_C;Accession: A35616 R;Aruffo, A.; Stamenkovic, I.; Melnick, M.; Underhill, C. Cell 61, 1303-1313, 1990	A;Title: CD44 is the principal cell surface receptor for hyaluronate.  A;Reference number: A35616; MUID:90304889; PMID:1694723 A;Accession: A35616 A;Status: nucleic acid sequence not shown; not compared with conceptual
OY 897 GCTCTGCTAGTGCTCTCTTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTAT		Qy 957 GTCAAAAGGTATGTGAAGGCCTTCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATC	Qy         1017 GAAACCAAAGTAGTAAAGGAGGAGAGAGCCAATGATGATGAACCCTAATGAG           Db         304 IleAsnAsnGlvAsnGlvAlaValGluAsnArdlvaSerSerGluIenIAsnGluGlu	GAATCAAAGAAAACTGATAAAACCCAGAAGAGTCCAAGGCCCAAGC	Qy 1116 AAA 1118 ::: Db 343 Gln 343		CD44 membrane glycoprotein precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 01-Dec-2000 C;Accession: A34424; A34907 R;Nottenburg, C; Rees, G; St. John, T.	Proc. Natl. Acad. Sci. U.S.A. 86, 8521-8525, 1989 A,Title: Isolation of mouse CD44 cDNA: structural features are distinct fro A,Reference number: A34424; MUID:90046829; PMID:2682651 A,Accession: A34424	A,Status: preliminary A,Molecule type: mRNA A,Residues: 1-365 <not> A,Cross-references: GB:M27130; NID:q192530; PIDN:AAA37407.1; PID:q309161</not>	R.Wolffe, E.J.; Gause, W.C.; Pelfrey, C.M.; Holland, S.M.; Steinberg, A.D.; J. Biol. Chem. 265, 341-347, 1990 A.Fitile: The CDNA sequence of muuse Pgp-1 and homology to human CD44 cell s.A.Reference number: A34907; MUID:90094420; PMID:2403559	A;Accession: A440/ A;Status: preliminary A;Molecule type: mRNA A;Residues: 8-195,'G',197-365 <wol></wol>	A;Cross.references: GB:JO5163; NID:g200334; PIDN:AAA39923.1; PID:g200335 C;Superfamily: human cell adhesion protein CD44 C;Keywords: cell adhesion; glycoprotein; membrane protein	Alignment Scores: 2.89e-11 Length: 365 Pred. No.: 222.50 Matches: 88 Score: 40.11* Conservative: 56	: 24.51% Mismatches: 6.17% Indels: 2 Gaps:	US-10-079-111-2 (1-2029) x A34424 (1-365)	Qy 225 TGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGG	Qy 270 CTTTCCAGGTGTCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAAC :::	

Alignment Scores Pred. No.: Score: Percent Similari Best Local Simil Query Match:	Scores: milarity: Similarity: h:	8.01e-11 217.50 38.73\$ 25.43\$ 6.03\$	Length: Matches: Conservative: Mismatches: Indels: Gaps:	362 88 46 61 13	
US-10-079-	-111-2 (1-2029	9) x A35616 (1-3	362)		
à i		GCAGAAGAGCTTTCC	ATCCAGGTGTCATGC	TCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCTT	311
		HisGluGlnIleAsp	LeuAsnIleThrCys <i>l</i>	ArgTyrAlaGlyValPheHis	37
 \$ 5	312 GTGAGCAAA         38 ValGluiws	AAGGCGAACCAGCAG AspGlvargtvrger	CTGAATTTCACAGAAC	GTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTG	371
		AGTTTGGCCGGCAAG		ATAMIANS PUCCOS SCIENTS SCIENTS	37
	ω	:::    ThrLeuProThrMet	:::  AspGlnMetValMetA	PheAsnSerThrLeuProThrMetAspGlnMetValMetAlaLeuSerLysGlyPheGlu	77
γ	432 ACTTGCAGC	TATGCTGGGTTGGA	GATGGATTCGTGGTC?	ACTIGCAGCIAIGGCIGGGIIGGAGGAIIGGACIGGICGICGICAICICIAAGAIIAGCCCCAAAC	491
Dβ	78 ThrCysArg	TyrdlyPheile	GluGlyHisValval	[leProArglleGlnProAsn	96
	0 1	GGGAAAATGGGGTG	GGTGTCCTGATTTGG	CCCAAGTGTGGGAAAAATGGGGGTGGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAG	551
	<u>,                                    </u>	AlaAlaAsnHı s'Thr	GlyValTyrIleLeu1	hrSerAsnThrSerHis	115
		TATTGTTACAACTCA	tctgatacttggact/ 	TTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATT	611
	116 TyrAspThr	TyrCysPheAsnAla	SerAlaProLeuGluC	luAspĊys	131
	C)	AAAGATCCCATATTC :::	aacactcaaactgcaa     :::	ATCACCACCAAAAGATCCCATATTCAACACTCAAACTGCAACCAAAACAACAAGAATTTATT	671
Db 1	132Thrser	ValThrAspLeuPro	AsnSerPheGluGlyE	-ThrSerValThrAspLeuProAsnSerPheGluGlyProValThrIleThrIleVal	150
	672 GTCAGTGAC	AGTACCTACTCG	GTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACA	CTACAATA	716
		Glyfhrargfyrser	LysLysGlyGluTyr <i>l</i>	AsnArgAspGlyThrArgTyrSerLysLysGlyGluTyrArgThrHisGlnGluAspile	170
		CCTGCCCCTACTACTCCTCCTGCTCCAGCTTCC	GCTCCAGCTTCC	CCTGCCCCTACTACTACTCCTGCTCCAGCTTCC	752
	171 AspAlaSer	AsnThrThrAspAsp	AspvalSerSerGlyS	erSerSerGluLysSerThr	190
δλ	753	ACT	TCTATTCCACGGAGA	ACTICIATICCACGGAGAAAAAATIGAITIGIGICACA	791
Db 3	191 SerGlyGly	TyrValPheHisThr	TyrLeuProThrIle	erGlyGlyTyrValPheHisThrTyrLeuProThrIleHisSerThrAlaAspGlnAsp	210
λ	792 GAAGITITI	ATGGAAACTAGCACC	ATGTCTACAGAA	GAAGITITITATGGAAACTAGCACCATGTCTACAGAA	827
Dp 7	211 AspProTyr	PhelleGlySerThr	MetAlaThrArgAspC	lnAspSerSerMetAspPro	230
ζζ	828		<u> </u>	-ACTGAACCATTTGTTGAAAAT	848
Dp 5	231 ArgGlyAsn	SerLeuThrValThr	AspGlySerLysLeul	ArgGlyAsnSerLeuThrValThrAspGlySerLysLeuThrGlyHisSerSerGlyAsn	250
š	849 AAAGCAGCA	TTCAAGAATGAAGCT	AAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGA	GGTGTCCCCACGGCT	668
Dp qu	251 GlnAspSer	GlyAlaAsnThrThr	serArgProGlyArgl	GinaspSerGlyAlaAsnThrThrSerArgProGlyArgLysProGlnIleProGluTrp	270
ζ	900 CTGCTAGTG	CTTGCTCTCTCTTC	TTTGGTGCTGCAGCT(	CTGCTAGTGCTTGCTCTCTTTTGGTGCTGCTGGTCTTGGATTTTGCTATGTC	959
da	271 LeuileVal	LeuAlaSerLeu	eulleValLeuAlaSerLeuLeuAlaLeuAlaLeuIleLeuAlaValCys	leleuAlaValCys	287
ò	960 AAAAGGTAT	GTGAAGGCCTTCCCT	TTTACAAACAAGAATC	AAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGGAA	1019
Db	288	iieAlaValAsnSer	ArgArgArgCysGlyC	-IleAlaValAsnSerArgArgArgCysGlyGlnLysLysLysLeuVallle	304
н	20	GTAAAGGAGGAGAAG	GCCAATGATAGCAACC	ACCADAGTAGTAAAGGAGAGAAGGCCAATGATGGAACCCTAATGAGGAATCAAAGAAA	1079
gr	305 Asnser	GiyasnGiyLys	ValGluAspArgLysE	roSerGluLeuAsnGlyGlu	322

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Tymphocyte homing receptor isoform CD44 - human C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) Septimental Septiments (man) Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septimental Septime
   --GAGTCCAAGAGTCCAAGCAAACTACCGTG 1127
                                     323 AlaSerLysSerGlnGluMetValHisLeuValAsnLysGluProSerGluThrProAsp 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGCGIGCAGAAGAGCTTICCAICCAGGIGICAIGCAGAATTAIGGGGAICACCCTIGIG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 CysArgTyrGlyPheIle---GluGlyHisValValIleProArgIleHisProAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 AsnSerThrLeuProThrMetAlaGlnMetGluLysAlaLeuSerIleGlyPheGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 IleCysAlaAlaAsnAsnThrGlyValTyrIleLeuThrSerAsnThrSer---GlnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||||:::|||:::|||
115 AspThrTyrCysPheAsnAlaSerAlaProProGluGluAspCysThrSerValThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 AGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495 AAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 LeuProAsnAlaPheAspGlyProlleThrlleThrIleValAsnArgAspGlyThrArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 GCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT------
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1110
76
178
1183
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Matches:
Conservative:
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                                                                                                                 1128 CGATGCCTGGAAGCTGAA 1145
                                                                                                                                                       ::: ::: | | | ::: 343 GlnPheMetThrAlaAsp 348
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215.50
34.00%
20.11%
5.98%
1080 ACTGATAAAAACCCAGAA
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Best Local Similarity:
Query Match:
DB:
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All ternate names: CD44 procursor - bovine
NiAlternate names: CD44 protein
Cilsecies: Bos primigenius taurus (cattle)
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Cipsecies: Bos primigenius taurus (cattle)
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Ribin, T.; St John, T.; Gallatin, W.M.; Harp, J.A.
Ribinmuch. 28, 1131-1135, 1991
A;Title: Sequence of the bovine CD44 cDNA: comparison with human and mouse sequences.
A;Reference number: A53286; MUID:92017904; PMID:1922105
A;Reference number: A53286, MUID:92017904; PMID:1922105
A;Residues: 1-56 cAB3
A;Residues: 1-56 cAB3
A;Residues: 1-56 cAB3
A;Residues: Cell adhesion protein CD44
C;Superfamily: human cell adhesion protein CD44
C;Superfamily: human cell adhesion; glycoprotein CD44
C;Reywords: cell adhesion; glycoprotein CD44
C;Reywords: cell adhesion; glycoprotein CD44
C;Reywords: cell adhesion; glycoprotein CD44
C;Reywords: cell adhesion glycoprotein CD44
F;21-366/Pomain: transmembrane #status predicted cYMN>
F;21-366/Pomain: transmembrane #status predicted cYMN>
F;25,57,100,110,120,222,260/Binding site: carbohydrate (Asn) (covalent) #status predicte
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495 AAGIGGGAAAAAAGGGGTGGGTGCTCTCATTTGGAAGGTTCCAGTGAGCGGACAGTTT 554	96 IleCysAlaAlaAsnAsnThrGlyValTyrIleLeuThrSerAsnThrSerGlnTyr 114	555 GCAGCCTATTGTTACAACTCATCTGGATACTTGGACTAACTCGTGCATT 602	115 AspThrTyrCysPheAsnAlaSerAlaProProGluGluAspCysThrSerValThrAsp 134	LeuProAsnAlaPheAspGlyProlleThrIleThrIleValAsnArgAspGlyThrArg	603CCAGAAATTATCACCACAAAGAT 632		633 ITCAACACTCAAACTGCAACACAAACAAAATTTATTGTCAGTGACAGTACCTACTCG 692	AspAspAspValSerSerGlySerSerGluArgSerSerThrSerGlyGlyTyr	693 GIGGCAICCCCTTACTCTACAATACCTGCCCCTACTACTACTCCTCCTGCT 743	TATG 80	:::::: 214 AspSerThrAspArg1leProAlaThrSerThr 224	804 GAAACTAGCACCATGTCTACAGAAACTGAACCAGTTTGTTGAAAATAAAGCAGCATTCAAG 863	225 SerSerAsnThrIleSerAlaGlyTrpGlubroAsnGluGluAsnGluAspGluArg 243		244 AspArgHisLeuSerPheSerGly 251	924 TITGGIGCIGCAGCIGGICTIGGATTITGCIATGTCAAAAGGTAIGIGAAGGCCTICCCT 983 252Serdlyll:: 254	+-1	::: :::       ::: ::: ::: ::: ::: ::: :	GCCAATGATAGCAACCCTAATGAGAATCAAAGAAAACTGATAAAAACCCAGAAGAGTCC	AlaPheAspHisThrLysGlnAsnGlnAspTrpThrGlnTrpAsnProSerHisSer 28	1104 AAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCTGAAGTTTAGATG 1154 200AAADDCGTTTAGATG 1154		306ArgAssnGlyThrThrAlaTyxGluGlyAsnTrpAsn 317	GTTGGGGAATTCAAAACGGGAAACGAAACAAACGAAAACAAAAAAAA		1275 GGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGCCCTTCTCT 1334	323	TATTGTAACCCTGTCTGGATCCTATCCTCCAAAGCTTCCCACGGCCTTTCTAG :::    :::    :::	HisserThrserThr11eglnAlaThrProSer	CCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGACC	347 347
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960 AAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAA 1019
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374
                                                                                                                                                                                  435 TGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATTAGCCCCAAACCCC 494
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C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: S13530
                                                                                                                                                                                                      --TCTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAG
                                                                             37 GluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAspLeuCysLysAlaPhe
                                                                                                                                     495 AAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCCGACAGTTT
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                                                                                                                  270 LeullelleLeuAlaSerLeu---LeuAlaLeuAlaLeuIleLeuAlaValCys-
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                                                                                                                                                                                                                                                                                                                                                 115 AspThrTyrCysPheAsnAlaSerAlaProProGluGluAspCys----
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                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 23-Nov-1991 #sequence revision 23-Nov-1991 #text_change 01-Dec-2000
C;Accession: JH0417; A32376; G02251; A32377
R;Harn, H.J.; Isola, N.; Cooper, D.L.
B;Aarn, H.J.; Isola, N.; Cooper, D.L.
Biochem: Biophys. Res. Commun. 178, 1127-1134, 1991
A;Title: The multispecific cell adhesion molecule CD44 is represented in reticulocyte A;Reference number: JH0417; MUID:91337049; PMID:1840487
                                                                                                                                 1622
                                                               1515 GTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACC 1574
                   380
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TAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGG
                                                                                                                                 1575 CTTTCTTCAGCTCTGAAAGAGAAACACGTATCCCAC------CTGACATGTCCT
                                                                                                                                                                381 ThrGlyThrAlaAlaAlaSerAlaHisThrSerHisProMetGlnGlyArgThrThrPro
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|-----ProLysGluAspSerHisSerThr
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;Residues: 1.108,'S',110-293,'S' <GOL>
;Cross-references: GB:MZ5078; NID:g186660; PIDN:AAA36138.1; PID:g186661
;Superfamily: human cell adhesion protein CD44
                                                                                                                                                                                                                      TCTGAGCCCGGTAAGAGCAAAAGAATGGCAGAAAAGTTTAGCCCC
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Mismatches:
Indels:
Gaps:
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Matches:
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AAGAATGAAGCTGCTGG	Db   309	1086 AAAACCCAGAAGAGTCCAAGCAAACAACTACCGTGCGATGCTGGAAGCTGAA 1086 AAAACCCAGAAGAGTCCAAGCAAGCAAAACTACCGTGCGATGCCTGGAAGCTGAA 1349 ValAsnArgSerLeuSerGlyAspGlnAspThrPheHisProSerGlyGlySerHisT 1146 GTTTAGATGAAGAAATGAGGAGACACCTGAGGCTGGTTTCTTTC	CAAAGAACCAAAGAAAGTCCA 31yalaAsnThrThrSerGlyProlleArgT AGGACTGCCATTGGACTATGGAGTGCACCAA	1317 402 1377 409	TATCCAGTGGTAAAAAGGCC 1490  ::::        eAsnSerGlyAsnGlyAla 441	C;Date: 20-Oct-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000 C;Accession: S45305 C;Accession: S45305 C;Accession: S45305 C;Accession: S45305 C;Ailde, K.F.; Alejandro, R.; Mintz, D.H.; Pastori, R.L. Biochim. Biophys. Acta 1218, 112-114, 1994 A;Title: Molecular cloning of the canine CD44 antigen cDNA. A;Reference number: S45305, WUID:94250687; PMID:7514890 A;Accession: S45305 A;Accession: S	:. : :
RiStamenkovic, I.; Aruffo, A.; Amiot, M.; Seed, B. ENBO J. 10, 343-349, 1991 A/Title: The hematopoietic and epithelial forms of CD44 are distinct polypeptides with A;Reference number: S13530; MUID:91122041; PMID:1991450 A;Recession: S13530 A;Recession: S13530 A;Retus: preliminary A;Molecule type: mRNA A;Residues: 1-493 <sta> A;Coss-references: EMBL:X55150; NID:g29800; PIDN:CAA38951.1; PID:g29801 C;Keywords: transmembrane protein</sta>	Alignment Scores:  Pred. No.:  Score: Score: Score: Score: Score: Score: Alignment Scores: Score: Sc	-2 (1-2029) x S13530 (1-493)  TTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCTTGTG	375 375 57 435	77 CysargTyrGlyPhelleGludlyHisValValTieProArgileHisProArsnser 495 AAGTGGGGAAAARGGGGTGGGTGCTCARTTGGAAGGTTCCAGTGAGCGGTTT 495 AAGTGGGGAAAARGGGGTGGGTGCCTGATTTGGAAGGTTCCAGTGAGCGTTTTT	DD 115 ASPINITYTCYSPHEASINALASETALAPTOPTOGLUGIUASDCYSTHITSETVAITHTASP 134  QY 602	Qy         633 TTCAACACTCAAACTGCAACAACAACAACAAGAA	Qy 726 ACTACTACTCCTCCTGCTCCAGCTTCCATTCCACGGAGAAAAATTGATTTGT 785

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Alignment Scores:
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                                                                  345 ACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCCGGCAAGGACCAAGTT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAGGCTTGGAGATGGATTC 464
                                                                                                                                                                                                                                                                      20 ThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSerIleSerArg 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValvalileProArgileGlnProAsnAlaIleCysAlaAlaAsnHisThrGlyValTyr 98
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                                                                                                                                                                                                           285 TCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                      40 ThralaAlaAlaAspLeuCysLysAlaPheAsnSerThrLeuProThrMetAlaGlnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    525 ATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         585 TGGACTAACTCGTGCATTCCAGAAATTATCACCACAAAGATCCCATATTCAACACTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProGluGluAspCys------ThrSerValThrHisLeuProAsnAlaPhe
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|153 GluTyrArgThrAsnProGluAspIleAsnProSerAsnProThrAspAspAspValSer
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US-10-079-111-2 (1-2029) x S45305 (1-351)
                                                                                                                                    3 TrpGlyLeuCysLeuLeu-
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Nicricocyce and mains receptor (1944, $9); and con Code41, incode, cell surface (1) Alterente names: cell adhesion molecule core protein CD441; symphocyte homing receptor CD44, splice (com CD4411, symphocyte homing receptor CD44, splice (com CD4411, symphocyte homing receptor CD44, splice (com CD4411, symphocyte homing receptor CD44, splice (com CD4411, symphocyte homing receptor CD44, splice (com CD4411, symphocyte homing receptor CD44, splice (com CD4411, symphocyte homing receptor CD44, splice (com CD4411, symphocyte splice) (species non-commerce) 190519; M39203, M39203, M3432, C44421, M39223, S16447 (com CD4411, symphocyte splice) (species non-commerce) 190519; M39203, M39203, M3432, C44421, M39223, S16447 (com CD4411, symphocyte splice) (species non-commerce) 190519; M10193177999; PM10206274 (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice) (com CD4411, splice)
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981 -316 1029 -336 1086	Qy 1146 GTTTAGATGAGAAAATGA :: ::       Db 368 hrThrHisGlySerGluSerA Qy 1206 CCTGCCCCGAGCTGGGGAAATC	Db 378    :::  Qy 1259CCTTGGTTCCTAACTGG     :::    Db 395 hrProGlnIleProGluTr	RESULT 13 177371 CD455 - human C;Species: Homo sapiens (man) C;Date: 02-Aug-1996 #sequence_revi	C;Accession: 177371 R;Tanabe, K.K.; Nishi, T.; Saya, H Moll. Carcinog. 7, 212-220, 1993 A;Title: Novel variants of CD44 ar A;Reference number: 157483; MUID:9	A; Accession: 177371 A; Status: preliminary; translated f A; Molecule type: mRNA A; Residues: 1-395 < RES> A; Cross-references: GB: S66400; NID: C; Genetics:	A; Gene: GDB:CD44 A; Cross-references: GDB:120739; OW A; Map position: 11pter-11p13 A; Introns: 257/1 C; Superfamily: human cell adhesion	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Score: Best Local Similarity: 23.04% Query Match: DB:	1-2 (1-2029) 5 TTGCTGCAC     7 LeuSerLeu	Qy 315 AGCAAAAAGGCGAACCAGCAC Db 37 GluLysAsnGlyArgTyrSer Qy 375 GGACTAAGTTTGGCCGGCAAC Db 57 AsnSerThrLeubroThrMet Qy 435 TGCAGCTAIGGCTGGGTTGGA	Db 77 CysArgTyrGlyPhelle   Qy 495 AAGTGTGGGAAAATGGGGTC
Pred. No.: 1.75e-09   Length: 426	GCTG	375 GGALIAGACCAGGAAAGACAAAGACTIGAAACTIGAAACT 434	AAGTGTGGGAAAAATGGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTT	555 GCAGCCTATTGTTGTTACAACTCTGATACTTGGACTAACTCGTGCATT 602	135 LeuProAsnAlaPheAspGlyProlleThrIleThrIleValAsnArgAspGlyThrArg 154 603	633 TTCAACACTCAAACTGCAACACAACAACAAA	195 PheTyrThrPheSerThrValHisProlleProAspGluAspSerProTrpIleThrAsp 214 681 AGTACCTACTCGGTGGCATCCCCTTACTCTACATACCTGCCCCT 725         215 SerThrAspArglleProAlaThrAsnMetAspSerSerHisSerThrThrLeuGlnPro 234	726 ACTACTCCTCCTGCTCCAGCTTCCACTTCCAGGGGAAAAAATTGATTG	AATAAA	309Gludly Tyrthreerije 115
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rising from alternative splicing: changes in the CD44 a. 93356912; PMID:8352881
AGCAGAAGGAAATGATCGAAACCAAAGTA------ 1028
                                                                  CCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACTGAT 1085
                                                                                                                                      AGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCTGAA 1145
                                                                                                                                                                                                      SAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTAC 1205
                                                                                                                                                                                                                                                                            TCAAAAGGGCCAAAGAACCAAAGAAGAAGTCCA---- 1258
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rgThrPheIleProValThrSerAlaLysThrGlySerPhe 335
                                                                                                                                                                                                                                          rAspGlyHis----- 377
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rGlnGluGlyGlyAlaAsnThrThrSerGlyProlleArgT 395
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erileSerArgThrGluAlaAlaAspLeuCysLysAlaPhe
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Matches:
Conservative:
Mismatches:
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321 AAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTA 380 255 SerValProGluLysLeuThrPheGluGluAlaLysGluLeuCysArgLysArgAspGly 274 381 AGTTTGGCCGGCAAGGACCAAGTTGAAACGCTTGAAAGCTTGAAACTTGCAGC 440 275 ValLeuAlaSerValGlyAsnMetTyrValAlaTrpArgAsnGlyPheAspGlnCysAsp 294 441 TATGGCTGGGTTGGAAGTTGGTGCTTCTAGGATTAGCCCAAAGTGT 500	GGGAAAATGGGGTGCTCGTTT		987 ACAAACAATCAGCAAAGGAAATGATCGAAACCAAAGTAATAAAGGAGAGAGA	SHishsp
8 8 8 8 8		4 6 6 6	8 8 8 8 8	6 6 6 6 6 6 6 6
Qy         1026GTAGTAAAGGAGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT 1082           Db         306 GLyAlaValAspAspArgLysAlaSerGlyLeuAsnGlyGluAlaSerArgSerGln 324           Qy         1083 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAAGCT 1142           Db         325 GluMetValHisLeuValAsnLysGluSerSerGluThrGlnAspGlnPheMetThrAla 344           Qy         1143 GAA 1145           Bb         345 Asp 345	SULT 15 7171 ondroitin sulfat Species: Gallus Date: 21-Sep-199 Accession: A4717 Shinomura, T.; N Biol. Chem. 268 Shinomura, T.; N Biol. Chem. 268 Sinomura, T.; N Biol. Chem. 268 Coession: A4717 Scession: A4	Alignment Scores:  Pred. No.:  Pred. No.:  152.50  Matches:  Best Local Similarity:  Query Match:  2	ATCCGGATGTCTCGGTTATGAAGTGGAGCGGTGAGTGTGAGCCTC	

rattus norv rattus norv sapien mus musculu rattus norv oryctolagus homo sapien mus musculu homo sapien

homo

062059 P55067

P55068 Q9erb4 O14594

PGCB RAT
PGCV RAT
PGCN HUMAN

MOUSE

PGCV]

felis silve herpes simp mus musculu

> P06487 P55066

BRA1\_RAT LDL2\_XENLA PGCB\_FELCA VGLI\_HSV11 PGCN\_MOUSE ODP2\_MYCPN PLK\_HUMAN

Q99088 P41725

rattus norv xenopus lae

Q9esm2

taurus

soq

Q9gzv7 P81282

Q9esm3

PGCA\_RABIT
PGCV\_HUMAN
BRA1\_MOUSE
BRA1\_HUMAN
PGCV\_BOVIN

Q28670 P13611

gall mus musculu

gallus

homo sapien

P75392 P10915 P07354

mycoplasma

rattus norv

P03994

saccharomyc

Q9qup5 P25653 P55252 P36170

PLK\_RAT PLK\_MOUSE FIGZ\_YEAST PLK\_BOVIN

CHICK

KK82\_YEAST

saccharomyc

362 AA.

ALIGNMENTS

bos taurus

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90304889; PubMed=1694723;
Aruffo A., Stamenkovic I., Melnick M., Underhill C.B., Seed B.;
"CD44 is the principal cell surface receptor for hyaluronate.";
Cell 61:1303-1313(1990).
-!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
mucosal high endothelial venule and to types I and VI collagen.
Probably involved in matrix adhesion, lymphocyte activation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymph node homing.

-- SUBCELLULAR LOCATION: Type I membrane protein.

-- INDUCTION: By EBV.

-- PTM: Extensively modified including N- and O-linked glycosylation, addition of the glycosaminoglycan chondroitin sulfate, of sulfate, of phosphate to cytoplasmic domain serine residues.

-- SIMILARITY: Contains I link domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
(Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cricetulus griseus (Chinese hamster)
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 SEQUENCE FROM N.A.
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|||:::
---ThrSerValThrAspLeuProAsnSerPheGluGlyProValThrIleThrIleVal 150
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P26051; Q99021;
D14M21-1992 (Rel. 22, Created)
D1-NOV-1997 (Rel. 35, Last sequence update)
D1-NOV-1997 (Rel. 43, Last annotation update)
D244 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-1)
(Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
D0ming/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=91191552; PubMed=1707342;
MEDLINE=91191552; PubMed=1707342;
Meuchhert U., Hofmann M., Rudy W., Reber S., Zoeller M.,
Hausmann I., Matzku S., Wenzel A., Ponta H., Herrlich P.;
"A new variant of glycoprotein CD44 confers metastatic potential irat carcinoma cells.";
Cell 65:13-24(1991).
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|LeulleValLeuAlaSerLeu---LeuAlaLeuAlaLeuIleLeuAlaValCys-
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                                                                                                            PERINTS, PROJUSS, Alink, 1.

PRINTS; PRO0658; CD44.

PRINTS; PRO1058; Link, 1.

PRODOM; PRO00918; Link, 1.

SMART; SM00445; LINK; 1.

PROSITE; PS01241; LINK; 1.

PROSITE; PS01241; LINK; 1.

PROSITE; PS01241; LINK; 1.

PROSITE; PS01241; Alternative splicing; Phosphorylation; Receptor; Proteoglycan; Signal; Alternative splicing;
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InterPro; IPR001231; CD44 antigen.
InterPro; IPR000538; Link.
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leuGluGluAspCys------ThrSerValThrAspLeuProAsnSerPhe 143
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TrpGlyLeuLeuCysLeuLeuGlnLeuSerLeuAlaGlnGlnIleAspLeuAsnIle 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 AspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSerLysLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 GluTyrArgThrHisGlnGluAspileAspAlaSerAsnIleIleAspGluAspValSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 AsnProlleHisSerAsnProGluValLeuLeuGlnThrThrThrArgMetThrAspIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             933 GCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAG------GCCTTCCCTTTT
                    HNNHPSQRMTTQSQEDVSWTDFFDPISHPMGQGHQTESK
-> SDGDSSMDPRGGFDTVTHGSELA (in isoform
                                                           /FTId=VSP 005330.
R -> S (IN REF. 2).
FB489D009BD4EE22 CRC64;
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1126
60
242
86
                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                        MW.
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36.19%
24.51%
6.34%
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503 AA;
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Query Match:
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                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001231; CD44_antigen.
InterPro; IPR001339; Link.
Pfam; PP001931; Xlink; 1.
Prints; PR001265; LINKADDULE.
PRINTS; PR001265; LINKADDULE.
PROOF PR001918; Link; 1.
SMART; SM00445; LINK; 1.
PROSITE; PS01241; LINK; 1.
Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;
Proteoglycan; Signal; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IATTPWVSAHTKQNQERTQWNPIHSNPEVLLQTTTRMTDID
RNSTSAHGENWTQEPQPPFNNHEYQDEEETPHATSTTWADP
SEQUENCE FROM N.A. (ISOFORM 1).
Stevens J.W., Midura R.J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
                                                                                                                                                                              Name=1; Synonyms=Short;

Isold=P26051-2; Sequence=VSP 005330;

PTM: N-glycosylated (By similarity).

PTM: O-glycosylated; contains chondrolitin sulfate glycans which

can be more or less sulfated (By similarity).

PTM: Phosphorylated; activation of PKC results in the

dephosphorylation of Ser-467 (constitutive phosphorylation site),

and the phosphorylation of Ser-467 (constitutive phosphorylation site),

SIMILARITY: Contains 1 link domain.
                                                       mucosal high endothelial venule and to types I and Vi collagen. Probably involved in matrix adhesion, lymphocyte activation and lymph node howing.

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRROLIDONE CARBOXYLIC ACID (PROBABLE)
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(POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                           Event=Alternative splicing, Named isoforms=2,
    Comment=Additional isoforms seem to exist;
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                                                                                                                                                       Name=2; Synonyms=Long, Meta-1;
IsoId=P26051-1; Sequence=Displayed;
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EMBL; M61874; AAA53534.1; -.
EMBL; US2179; AAA97915.1; -.
EMBL; U46957; AAA92920.1; -.
PIR; B38745; B38745.
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                                    284 AsnAsnHisGluTyrGlnAspGluGluThrProHisAlaThrSerThrThrTrpAla 303
                                                                                                                   304 AspProAsnSerThrThrGluGluAlaAlaThrGlnLysGluLysTrpPheGluAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SerSerGly---Asn
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                                                                              GAAACCAAAGTAGTAAAGGAGGAGAAAGCCCAATGATAGCAACCTAATGAGGAATCAAAG
                                                                                                                                                                                               324 TrpGlnGlyLysAsnProProThrProSerGluAspSerHisValThrGluGlyThrThr
                                                                                                                                                          1077 AAAACTGATAAAAACCCA-----GAAGAGTCCAAGAGTCCAAGAGTACCC
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01-APR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
CD44 antigen precursor (Phagocytic apycoprotein I) (PGP-1) (HUTCH-I)
(Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
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BEDLINE-89282830, PubMed=2471974;

Idzerda R.L., Carter W.G., Nottenburg C., Wayner E.A.,

Gallatin W.M., St John T.;

"Isolation and DNA sequence of a CDNA clone encoding a lymphocyte adhesion receptor for high endothelium ";

Proc. Natl. Acad. Sci. U.S.A. 86:4659-4663 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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NCBI_TaxID=9557;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteoglycan; Transmembrane; Glycoprotein; Phosphorylation; Receptor; Proteoglycan; Signal; Alternative splicing; Pyrrolidone carboxylic acid. SIGNAL
                                                             lymph node homing.

SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: Type I membrane protein.

Addition of the glycosaminoglycan chondroitin sulfate, of sulfate, of phosphate to cytoplasmic domain serine residues.

SIMILARITY: Contains I link domain.
FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
                  mucosal high endothelial venule and to types I and VI collagen. Probably involved in matrix adhesion, lymphocyte activation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY
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578BFCE7C3D52FFF CRC64;
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EXTRACELLULAR (POTENTIAL)
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Mismatches:
Indels:
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InterPro; IPR001538; Link.
Pfam; PF00193; Xink; 1.
PRINTS; PR00658; CD44.
PRINTS; PR01265; LINKMODULE.
ProDom; PD000918; Link; 1.
PROSITE; PR0144; LINK; 1.
PROSITE; PR0144; LINK; 1.
PROSITE; PR0144; LINK; 1.
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HSSP; P98066; 1TSG.
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GCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAA 419
                                                                    GCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATTCGTGGTCATCTTTAGG 479
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                      72 IleGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHisValValIleProArg
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P16070; P22511; Q04858; Q13419; Q13957; Q13958; Q13959; Q13960;
Q13961; Q13967; Q13968; Q13980; Q15861; Q16064; Q16065; Q16066;
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TISSUE=Breast carcinoma, MEDLINE=93356912; PubMed=8352881; Tanabe K.K., Nishi T., Saya H.; Tanabe K.K., Nishi T., Saya H.; "Novel variants of CD44 arising from alternative splicing: changes in the CD44 alternative splicing pattern of MCF-7 breast carcinoma cells
                       01-APR-1990 (Rel. 14, Created)
01-NOV-1997 (Rel. 15, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 41) (Horagocytic glycoprotein I) (PGP-1) (HUTCH-I)
(Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)
(Heparan sulfate proteoglycan) (Epican) (CDW44).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic structure of DNA encoding the lymphocyte homing receptor CD44 reveals at least 12 alternatively spliced exons."; Proc. Natl. Acad. Sci. U.S.A. 89:12160-12164(1992).
                                                                                                                                                                                                                                                                                                                             Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Н.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.G., Cornelis F.B., Gerth
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                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Alymphocyte molecule implicated in lymph node homing is
the cartilage link protein family.";
Cell 56:1057-1062(1989).
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MEDLINE-93101687; Pubmed-1465456;
Screaton G.R., Bell M.V., Jackson
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MEDLINE-91277598; PubMed=2056274;
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Q16208; Q16522; Q96J24;
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TISSUE=Reticulocytes;
                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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MEDINE-218825; PubMed=12477932;

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MEDINE-218825; PubMed=12477932;

MALSCHIE R.D., Collins F.S., Wagner L.H., Derge J.G.,

MALSCHIE S.P., Collins F.S., Wagner L.H., Schaefer C.F., Bhat N.K.,

MALSCHIE S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MALSCHIE S.P., Jordan H., Moore T., Max S.I., Wang J., Haiph F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MALSCHIE S., Morley K., Former A.P., Rabin G.P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MARINGAR S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Milalon D.K., Muzzy D.M., Sodergren E.J., Lu X., Glabs R.A.,

Milalon D.K., Mazzy D.M., Sodergren E.J., Lu X., Glabs R.A.,

Milalon D.K., Mazzy D.M., Sodergren E.J., Lu X., Glabs R.A.,

Milalon D.K., Mazzy D.W., Sodergren E.J., Lu X., Glabs R.A.,

Milalon D.K., Mazzy D.W., Sodergren E.J., Lu X., Glabs R.A.,

Milalon D.K., Mazzy D.W., Schwutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.M. Krzywinski M.I., Skalska U., Smailus D.E.,

M. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "CD44 splice variants confer metastatic behavior in rats: homologous sequences are expressed in human tumor cell lines.";
          Goldstein L.A., Zhou D.F.H., Picker L.J., Minty C.N., Bargatze R.F., Ding J.F., Butcher E.C.;
"A human lymphocyte homing receptor, the hermes antigen, is related to cartilage proteoglycan core and link proteins.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 223-265 FROM N.A.
MEDLINE-94198700; PubMed=8148709;
MATSHEMULA Y., Hanbury D., Smith J., Tarin D.;
"Non-invasive detection of malignancy by identification of unusual
CD44 gene activity in exfoliated cancer cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hofmann M., Rudy W., Zoeller M., Toelg C., Ponta H., Herrlich P.,
Guenthert U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Foreskin;
MEDLINE=91177958; PubMed=2007624;
MEDLINE=91177958; PubMed=2007624;
Brown T.A., Bouchard T., St John T., Wayner E., Carter W.G.;
"Human keratinocytes express a new CD44 core protein (CD44B) as heparan-sulfate intrinsic membrane proteoglycan with additional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 184-222 AND 473-625 FROM N.A. (ISOFORM KERATINOCYTE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Lymphoblast;

BubMed=1922057;

Shtivelman E., Bishop J.M.;

"Expression of CD44 is repressed in neuroblastoma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22399881; PubMed=12511867;
Ponta H., Sherman L., Herrlich P.A.;
"CD44: Erom adhesion molecules to signalling regulators.";
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Bosch P.P., Stevens J.W., Buckwalter J.A., Midura R.J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVIEW ON FUNCTION AND POST-TRANSLATIONAL MODIFICATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                           SEQUENCE FROM N.A. (ISOFORM WITHOUT EXON 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell. Biol. 11:5446-5453(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92005448; PubMed=1717145;
MEDLINE=89168435; PubMed=2466576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell Biol. 113:207-221(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer Res. 51:5292-5297(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 267-603 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-22 FROM N.A.
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And a blood group-related polymorphism of CD44 abolishes a hyaluronan-
RT binding consensus sequence without preventing hyaluronan binding.";

Biol. Chem. 271:147-7153 (1996).

E biol. Chem. 271:147-7153 (1996).

CC --- FUNCTION: Receptor for hyaluronic acid (HA). Mediates cell-cell
and ocell-matrix interactions through its affinity for HA, and
possibly also through its affinity for other ligands such as
cc osteopontin, collagens, and matrix matalloproteinases (MMPS).

CC osteopontin, collagens, and matrix matalloproteinases (MMPS).

CC recirculation and homing, and in hematopoiesis. Altered expression
or dysfunction causes numerous pathogenic phenotypes. Grace
protein heterogeneity due to numerous alternative splicing and
cc protein heterogeneity due to numerous alternative splicing and
cc protein heterogeneity and in hematogenic phenotypes. Grace
collagen, laminh, and fibronectin via its N-Cerminal segment.

CC --- SUBUNIT: Interacts with HA, as well as other glycosaminoglycans,
collagen, laminh, and fibronectin via its N-Cerminal segment.

MSN), and NF2 via its C-terminal segment.

CC --- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 TTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCTTGTG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 AsnSerThrLeuProThrMetAlaGlnMetGluLysAlaLeuSerIleGlyPheGluThr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 AGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 GluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAspLeuCysLysAlaPhe
                                                                                                                                                                                                                                                                                                 MEDLINE=22038351; PubMed=12032545; Legg J.W., Lewis C.A., Parsons M., Ng T., Isacke C.M.; Legg J.W., Lewis C.A., Parsons M., Ng T., Isacke C.M.; Anovel PKC-regulated mechanism controls CD44 ezrin association and directional cell mortlity,"; Anovel PKC-regulation (2002).
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Comment-Additional isoforms seem to exist. Additional isoforms
are produced by alternative splicing of 10 out of 19 exons
within the extracellular domain. Additional diversity is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bartolazzi A.;
"CD44s adhesive function spontaneous and PMA-inducible CD44 cleavage
are regulated at post-translational level in cells of melanocytic
                                                                                               cell migration can be blocked by a CD44 bide containing a phosphoserine at position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT BLOOD GROUP INDIAN PRO-46.
MEDLINE=96215152; PubMed=8636151;
Telen M.J., Udani M., Washington M.K., Levesque M.C., Lloyd E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      742
116
63
176
2203
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22766015; PubMed=12883358;
PHOSPHORYLATION OF SER-706.

BENDLINES-828484845; PubMed=9580567;
Peck D., Isacke C.M.;
"Hyaluronan-dependent cell migration"
                                                                                                                                                                     J. Ceil Sci. 111:1595-1601(1998).
[17]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Melanoma Res. 13:325-337(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOSYLATION AND PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.45e-11
                                                                                                                                     cytoplasmic domain peptide
                                                                                                                                                                                                                                                                        PHOSPHORYLATION OF SER-672
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20.79%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lineage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rao N.;
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1272 366 1332 379 1392 390	1452 391 1512 408 1572 423	RESULT 5 CD4 MESAU CD4 MESAU ID 7014 MESAU AC Q6052; Q6052; DT 01-NOV-1997 (Rel. 35, DT 15-MAR-2004 (Rel. 35, DT 15-MAR-2004 (Rel. 43, DE CD4 antigen precursor DE (Extracellular matrix DE homing/adhesion recept DE Heparan sulfate prote GN MESOCricetus auratus (S) Mesocricetus auratus (C)	Eukaryota; Mammalia; Eut Mammalia; Eut Mesocricetus. NCBL TaxID=10 SEQUENCE FROM STRAIN=1NG; Y Paulauskis J. Submitted (JUTO): FUNCTION: FUNCTION: SUBCELLUI SUBCELLUI ALTERNATI	CC Name=1; CC Name=1; CC Name=1; CC Name=2; CC ISOId=06052-1; CC ISOId=06052-2; CC I- PTM: N-glycosylate CC I- PTM: O-glycosylate CC I- PTM: D-glycosylate CC I- PTM: Phosphorylate CC I- STMILARITY: Contain CC I- SIMILARITY: Contain CC Name=1;
435 TGCAGCTATGGCTGGGTTGGAGTTCGTGGTCATCTTAGGATTAGCCCAAACCCC 494  77 CysArgTyrG1yPhelleGluGlyHisValVallleProArglleHisProAsnSer 95  495 AAGTGGGGAAAAAATGGGGTGCTGCTGATTTGGAAGGTTCCAGTGAGCCGACGTTT 554	LeuProAsnalaPheAspGlyProlleThrIleThrIleValAsnArgAspGlyThrArg	194 ilePheTyrThribieTH	906 GTGCTTGCTCTTTTGGTGCTGCTGGTCTTTGCTATGCTA	1080
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TCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGCCCTTCT 1331
                                                                                                                   CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTC 1391
                                                                                                                                                                                                                                                                                                                                                           CTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAG 1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTCTGAAAGAGAAACACGTATCCCAC------CTGACATGT 1619
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                                                                                                                                                                                                                                       IGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGG 1451
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---GlyTyrArgGlnThr-----ProArgGluAspSerHisSer 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaAlaAlaSerAlaHisThrSerHisProMetGlnGlyArgThrThr 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOFORMS 1 AND 2).
Liveolar macrophage (Atler M., Godleski J.J.;
zik L., Gerard C., Fatler M., Godleski J.J.;
to the EMBL/GenBank/DDBJ databases.
ell surface receptor for hyaluronate. Adhesion to othelial venule and to types I and VI collagen.
d in matrix adhesion, lymphocyte activation and
                                                                                                                                                         :::||| :::|||:::
---ThrSerThrIleGlnAlaThrProSer----
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ted (By similarity).

ted; contains chondroitin sulfate glycans which ess sulfated (By similarity).

ted; activation of PKC results in the n of Ser-395 (constitutive phosphorylation site), ylation of Ser-361 (By similarity).
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, Last annotation update)
or (Phagocytic glycoprotein I) (FGP-1) (HUTCH-I)
or receptor-III) (ECMR-III) (GP90 lymphocyte
ptor) (Hermes antigen) (Hyaluronate receptor)
teoglycan) (HAMI antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Golden hamster).
Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTAAGAGCAAAAGAATGGCAGAAAAGTTTAGCCCC 1667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.
:ION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splicing, Named isoforms=2;
onal isoforms seem to exist;
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191 SerGlyGlyTyrValPheHisThrTyrLeuProThrIleHisSerThrAlaAspGlnAsp 210
                                                           97 AlaIleCysAlaAlaAsnHisThrGlyValTyrIleLeuThrSerAsnThrSer---His 115
                                                                                                                                                                                                                                                                                612 ATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAACAACAACAGAATTTATT 671
                                                                                                                                                                                                                                 151 AsnArgAspGlyThrArgTyrSerLysLysGlyGluTyrArgThrHisGlnGluAspIle 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             912 GCTCTCCTCCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 GlyvalPheGlyGluThrGluValThrValAlaGluAspSerAsnPheAsnValAspGly 287
    78 ThrCysArgTyrGlyPheIle---GluGlyHisValValIleProArgIleGlnProAsn 96
                               #92 CCCAAGTGTGGGAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAG 551
                                                                                                                                                                                                                                                                                                                                                                                                                                    852 GCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCCACGGCTCTGCTAGTGCTT 911
                                                                                        552 TTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATT
                                                                                                                                                                 |||:::
---ThrSerValThrAspLeuProAsnSerPheGluGlyProValThrIleThrIleVal
                                                                                                                                                                                                                                                                                                                    ----ACTTCTATTCCACGGAGAAAAAATTGATTTGTGTCACA
                                                                                                                                                                                                                                                                                                                                                                             792 GAAGTTTTTAFGGAAACTAGCACCAFGTCTACAGAAACTGAAACTTTGTTGAAAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GluglyTyrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 ThrHisTyrProGluThrMetGluAsnGlyThrLeuThrProValThrProAlaLysThr
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P15379; Q05732; Q61395; Q62060; Q62061; Q62062; Q62063; Q62408; Q62409; Q64299; Q64299; Q62914; Q924X8; Q62409; Q64290 (Rel. 14, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
15-MRA-2004 (Rel. 43, Last annotation update)
CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I) (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 4; 6; 7 AND 12).
STRAIN=DBA/2; TISSUB=Lung;
STRAIN=B3107170; PubMed=146958;
He Q., Leeley J., Hyman R., Ishihara K., Kincade P.W.;
"Molecular isoforms of murine CD44 and evidence that the membrane
                                                                                                                 116 TyrAspThrTyrCysPheAsnAlaSerAlaProLeuGluGluAspCys-----
                                                                                                                                                                                                       672 GTCAGTGACAGTACC---TACTCGGTGGCATCCCCTTACTCTACA---
                                                                                                                                                                                                                                                                                                                                                                                            ::: ::: :::
211 AspProTyrPheIleGlySerThrMetAlaThr-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 SerGlyGlyLysAspGlyArgArgGly---GlyGlyLeuProLys--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAACCAAAGTAGTAAAGGAGAGAGAGGCCAAT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    972 AAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCAACCCTAATGAGGAATCAAAGAAAACTGAT 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 SerLeuProGlyAspGlnAspSerSerMetAsp 298
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                              PROSITE; PS01241; LINK; 1.
Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor; Proteoglycan; Signal; Alternative splicing;
Pyrrolidone carboxylic acid.
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MEDLINE=2288288 R.L., Felingold E.A., Grouse L.H., Derge J.G.,
MEDLINE R.P., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,
MEDLINE R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,
MEDLINE R.P., Jordan H., Moore T., Mars J., Mang J.,
MEDLINE S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
MEDRA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
MEDRA S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
MILLON D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
MILTETRIEL A.C., Grimwood J., Schmutz J., Myers R.M.,
MILTETRIEL A., Schein J.E., Jones S.J.M., Marra M.A.;
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MEDILE-90046829; PubMed=268551;
Nottenburg C., Ress G., St John T.;
"Isolation of mouse CD44 cDNA: structural features are distinct from Wittig B.M., Johansson B., Zoeller M., Schwaerzler C., Guenthert U.; "Abrogation of experimental collitis correlates with increased appoptosis in mice deficient for CD44 variant exon 7 (CD44v7)."; J. Exp. Med. 191:2053-2064(2000). "Molecular cloning and expression of Pgp-1. The mouse homolog of the MEDLINE=90038499; PubMed=2681416; Zhou D.F.H., Ding J.F., Picker L.J., Bargatze R.F., Butcher E.C., Goeddel D.V.; for hyaluronate recognition."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). human H-CAM (Hermes) lymphocyte homing receptor."; J. Immunol. 143:3390-3395(1989). Proc. Natl. Acad. Sci. U.S.A. 86:8521-8525(1989). STRAIN=C57BL/6J; TISSUE=Embryo; MEDLINE=22354683; PubMed=12466851; oximal domain is not critical for Cell Biol, 119:1711-1719(1992). SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE=20318634; PubMed=10859330; SEQUENCE FROM N.A. (ISOFORM 13). SEQUENCE FROM N.A. (ISOFORM 13) cDNA sequences. primate cDNA. and mouse proximal 

Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayshilzaki Y., "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDMAR." Yu Q., Toole B.P.;
"A new alternatively spliced exon between v9 and v10 provides a molecular basis for synthesis of soluble CD44.";
J. Biol. Chem. 271:20603-20607(1996)
-!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to mucosal high endothelial venule and to types I and VI collagen. Probably involved in matrix adhesion, lymphocyte activation and STRAIN=BALB/c; MEDLINE=93286043; PubMed=8509359; Screaton G.R., Bell M.V., Bell J.I., Jackson D.G.; Screaton G.R., Bell M.V., Bell J.I., Jackson D.G.; The identification of a new alternative exon with highly restricted tissue expression in transcripts encoding the mouse Pgp-1 (CD44) thoming receptor. Comparison of all 10 variable exons between mouse, Wolffe E.J., Gause W.C., Pelfrey C.M., Holland S.M., Steinberg A.D., "The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell surface antigen and proteoglycan core/link proteins."; J. Biol. Chem. 265:341-347(1990). SEQUENCE OF 224-637 FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7 AND MEDLINE=93219085; PubMed=8464707; Toelg C., Hofmann M., Herrlich P., Ponta H.; "Splicing choice from ten variant exons establishes CD44 IsoId=P15379-10; Sequence=VSP 007330, VSP 007334; IsoId=P15379-12; Sequence=VSP\_007336, VSP\_007337; VSP\_007339; VSP 007335; Event=Alternative splicing; Named isoforms=13; SÜBÜELLULAR LOCATION: Type I membrane protein. ALTERNATIVE PRODUCTS: PARTIAL SEQUENCE FROM N.A. (ISOFORMS 10 AND 11) IsoId=P15379-11; Sequence=VSP 007332, IsoId=P15379-13; Sequence=VSP\_007338, Name=6; Synonyms=M3; \_\_\_\_Squence=VSP\_005326; IsoLd=P15379-5; Squence=VSP\_005326; Name=7; Synonyms=M4; Isold=P15379-6; Sequence=VSP\_005327; IsoId=P15379-14; Sequence=Displayed; Name=2; IsoId=P15379-7; Sequence=VSP\_007329; :sold=P15379-8; Sequence=VSP\_007330; IsoId=P15379-4; Sequence=VSP\_007331; IsoId=P15379-9; Sequence=VSP\_007332; Name=12; Synonyms=M1; IsoId=P15379-3; Sequence=VSP\_005328; SEQUENCE OF 224-637 FROM N.A. (ISOFORM 9) (ISOFORM 13). vařiabilíty."; Nucleic Acids Res. 21:1225-1229(1993). Biol. Chem. 268:12235-12238(1993) 8-778 FROM N.A. (ISOF()4420; PubMed=2403559; MEDLINE=96355396; PubMed=8702806; 60,770 full-length cDNAs."; Nature 420:563-573(2002). Name=13; Synonyms=M0; Synonyms=M2; .ymph node homing. STRAIN=Swiss Webster; SEQUENCE OF 8-778 MEDLINE=90094420; and rat. August J.T.; Name=4; Name=10; Name=11; Name=1; Name=9; Name=8; STRAIN=GR; human, 

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                   AsnSerPheAspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSer 159
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-!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to mucosal high endothelial venule and to types I and VI collagen.

Probably involved in matrix adhesion, lymphocyte activation and lymph node homing.
-!- SUBSCELLULAR LOCATION: Type I membrane protein.
-!- TISSUB SPECIFICITY: Mesenteric lymph node and liver, not in heart.
-!- PIN: Extensively modified including N- and O-linked glycosylation,
                                                                                             LysLysGlyGluTyrArgThrHisGlnGluAspileAspAlaSerAsnIleIleAspAsp
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 41, Last annotation update)
17-MAR-2004 (Rel. 41, Last annotation update)
(Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
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ammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
WCBI_TaxID=9913;
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BOSWOCTH B.T., St. DubMed=1922105;
BOSWOCTH B.T., St. Dohn T., Gallatin W.M., Harp J.A.;
"Sequence of the bovine CD44 cDNA: comparison with human and mouse
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                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
             PTM: N-glycosylated (By similarity).
PTM: 0-glycosylated; contains chondroitin sulfate glycans which can be more or less sulfated (by similarity).
PTM: Phosphorylated, cativation of PKC results in the dephosphorylation of Ser-742 (constitutive phosphorylation site), and the phosphorylation of Ser-708 (by similarity).
POLYMORPHISM: Two allelic forms of this glycoprotein, PGP-1.1 and PGP-1.2, have been reported. The expressed product is PGP-1.1 (Ly-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 TrpHisThrAlaTrpGlyLeuCysLeuLeuGlnLeuSerLeuAlaHisGlnGlnIleAsp
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LeuAsnValThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 SerAlaProProGluGluAspCys-----ThrSerValThrAspLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 GATGGATTCGTGGTCATCTCTAGGATTAGCCCCAAACCCCAAGTGGGGAAAAATGGGGGTG
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EMBL; X66081; CAA46881.1; --
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EMBL; X66081; CAA46880.1; --
EMBL; X66081; CAA46880.1; --
EMBL; X71291; AAA37406.1; --
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X69724; CAA49380.1; -.
L13611; AAA37145.1; -.
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                                                                                                                                                              660 ACAGAATTTATTGTCAGTGACAGTACC---TACTCGGTGGCATCCCCTTACTCTACAATA 716
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    52 LeuCysLysAlaPheAsnSerThrLeuProThrMetAlaGlnMetGluAlaAlaArgAsn 71
                                                                                                                                                                                                                                                                                                                                                                                                                               72 IleGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHisValValIleProArg
                                                                                                                                  600 ATTCCAGAAATTATCACCACCAAAAATCCCATATTCAACACTCCAAACTGCAACACAAACA
                                                                                                                                                                                                                                                                                                                                                     -----ThrSerValThrAspLeuProAsnAlaPheGluGlyProlleThr
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                                             GCTAGCTTTGAAACTTGCAGCTATGCTTGGAGATGGATTCGTGGTCATCTTTAGG
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|165 ProGluAspIleAsnProSerValValSerProSerSerProProAspAspGluMetSer
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CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-1)
(Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canis familiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Pissipedia, Canidae, Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTICIATICCACGGAGAAAAAATIGATITGIGICACAGAAGIIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 35, Last sequence update)
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                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;
Proteoglycan; Signal; Alternative splicing;
    of sulfate,
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addition of the glycosaminoglycan chondroitin sulfate, of phosphate to cytoplasmic domain serine residues (By
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EXTRACELLULAR (POTENTIAL)
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InterPro; IPR000538; Link.
Pfam; PF00193; Xlink; 1.
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HSSP, P90066; 1TSG.
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PRINTS; PR01265; LINKMODULE.
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Indels:
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  Query Match:
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                                   STRAIN=Beagle; TISSUE=Thymus;

MEDLINE=94250687; PubMed=7514890;

Milde K.F., Alejandro R., Mintz D.H., Pastori R.L.;

Elophim. Biophys. Acta 1218:112-114(1994).

L. FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to mucosal high endothelial venule and to types I and VI collagen.

Probably involved in matrix adhesion, lymphocyte activation and lymph node homing.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

C.!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: Lymph nodes.

-!- FTM: Extensively modified including N- and O-linked glycosylation, addition of the glycosaminoglycan chondroitin sulfate, of sulfate, of plasmic domain serine residues (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0658; CD44.

PRINTS; PRO0658; CD44.

PRODOM; PRO1018; Link; 1.

SMART; SM00445; LINK; 1.

PROSITE; PS01241; LINK; 1.

PROSITE; PS01241; LINK; 1.

Proteoglycan; Signal; Alternative splicing;

Pyroclidone carboxylic acid.

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InterPro; IPR001231; CD44 antigen.
InterPro; IPR00538; Link.
Pfam; PF00193; Xlink; 1.
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à å	225	TGGACCACGAGGCTCCTGGTCC	AAGGCTCTTTGCGTGCP	
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Š f	285	TCATGCAGAATTATGGGGATCACCCT :::        Thr(vslrdrvalag)vValpheHi	£ 5	TGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTC 344
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ζ	405	GAAACAGCCTTGAAAGCTAGCT	TTGAAACTTGCAGCTAT	39
q	9			::::::  GlyPheIleGluGlyHis 78
ð £	465	GIGGICAICTCTAGGAITAGCCCAAACCCCAAGIGIGGAAAAIGGGGIGGGG	CAAACCCCAAGTGTGGG	SARARAGGGGGGGGGCCTG 524
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δλ	585	TGGACTAACTCGTGCATTCCAG	BAATTATCACCACCAAA	GATCCCATATTCAACACTCAA 644
qq	118	:::	::: ThrSerVal	::: ThrHisLeuProAsnAlaPhe 132
ζ	645	ACTGCAACACAACAACAAAT	TTATTGTCAGTGACAGT	AccTACTCGGTGGCATCC 701
q	133	AspGlyProlleThr1leThr1leValAsnArgAspGlyThrArgTyrSerGlnLy	:::  levalAsnArgAspGly	  ThrArgTyrSerGlnLysGly 152
ŏ	702	CCTTACTCTACAATACCTGCC-	-	CCTACTACTACTCCTCCTGCTCCAGCTTCC 752
qq	153	GluTyrArgThrAsnProGluAspIl	eAsn	  ProThrAspAspAspValSer 172
à	753	CTTCTATTCCACC	AATTGATTTGTGTCACA	GAAGTTTT 800
QΩ	173	SerGlySerSerSerGluArgSe	rThrSerAl	aGlyTyrAsnilePheHisThrHisLeu 192
ζò	801		- 1	-ATGGAAACTAGCACCATGTCTACAGAAACTGAA 833
qa	193	ProThrAlaTyrProThrGluA	ß	  ValSerSerAsnSerAspHis 212
δ	834		CCA	
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ò	858	TTCAAGAATGAAGCTGCTGGGTTT	1 1 1 1 1 1 1 1 1	
ф	233	HisGlySerGluSerAlaGlyH	SerSerGlyS	GluGlyGlyAlaAsnThrThr 252
δ	888		GTCCCCACGGCTCTG	CTAGTGCTTGCTCTCTTC 923
Db	253	SerGlyProMetArgLysProGl		:::::         IleIleLeuAlaSerLeu 271
ζŎ	924	TTTGGTGCTGCTGGTCTTG	GATTTTGCTATGTCAAA	AGGTATGTGAAGGCCTTCCCT 983
DÞ	272		.laValCysIleAla	283
Οy	984	TTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAAC	AGGAAATGATCGAAACC	CAAAGTAGTAAAGGAGAGAAG 1043
Db	284	:::: ValAsnSerArgA	:::::: erArgArgCysGlyGlnLys	  BLYSLYSLeuValIleAsnAsn 300
δ	1044	GCCAATGATA	GATAGCAACCCT	-AATGAGGAATCAAAGAAAACT 1082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
---AACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACC 1124
                    lymph node homing.
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- PTM: Extensively modified including N- and O-linked glycosylation, addition of the glycosaminoglycan chondroitin sulfate, of sulfate, of phosphate to cytoplasmic domain serine residues.
--- SIMILARITY: Contains 1 link domain.
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                                                                                                                                                                                                                  (PGP-1) (HUTCH-I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Main cell surface receptor for hyaluronate. Adhesion t mucosal high endothelial venule and to types I and VI collagen. Probably involved in matrix adhesion, lymphocyte activation and
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                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FBB-1994 (Rel. 43, Last annotation update)
CD44 antigen precursor (Pheorytic glycoprotein I) (PGP-1) (HUTCH (Extracellular matrix receptor-III) (GCMR-III) (GP90 lymphocyte homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)
                                                                                                                                                                                                                                                                                                              Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Perissodactyla; Equidae; Equus.
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MEDLINE=93170897; PubMed=8436424;
MEDLINE=93170897; PubMed=8436424;
Tavernor A.S., Deverson E.V., Coadwell W.J., Lunn D.P., Zhang C. Davis W., Butcher G.W.;
"Molecular cloning of equine CD44 cDNA by a COS cell expression
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PHOSPHORYLATION (BY PKC) (PARTIAL)
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Cell adhesion; Transmembrane; Glycoprotein; Proteoglycan; Signal; Alternative splicing; Pyrrolidone carboxylic acid.
BY SIGNAL
I 20 BY SIMILARITY.
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Interpro; IPR001231; Link.
Pfam; PP00193; Xlink; 1.
PRINTS; PR00558; CD44.
PRINTS; PR01255; LINKAWDDULE.
ProDom; PD000918; Link; 1.
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HSSP; P98066; 1TSG.
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1083 GATAAA--
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ID4 HORSE
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DT 011-FEB.
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115 AspThrTyrCysPheAsnAlaSerAlaProProGluGluAspCysThrSerValThrAsp
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PHOSPHORYLATION (PARTIAL)
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Matches:
Conservative:
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Indels:
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CALCIUM-BINDING (POTENTIAL)
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EGF-LIKE 2, CAI
C-TYPE LECTIN
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PRODOM; PRO00918; Link; 2.
PRACTO SMO0125; CCP, 1.
SMART; SMO0134; CCP, 1.
SMART; SMO0179; EGF CA; 1.
SMART; SMO0445; LINK; 2.
PROSITE; PSO0010; ASX HYDROXYL; 1.
PROSITE; PSO0010; ASX HYDROXYL; 1.
PROSITE; PSO0012; C_TYPE_LECTIN_1; 1.
PROSITE; PSO0014; C_TYPE_LECTIN_2; 1.
PROSITE; PSO1186; EGF L2; 1.
PROSITE; PSO1186; EGF L3; 1.
PROSITE; PSO1187; EGF L3; 1.
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InterPro; IPR001881; BGF 2.
InterPro; IPR001881; BGF Ca.
InterPro; IPR001309; BGF like.
InterPro; IPR003199; Ig-like.
InterPro; IPR003199; Ig-like.
InterPro; IPR003194; Lectin C.
InterPro; IPR000438; Link.
InterPro; IPR000438; Sushi_SCR_CCP.
Pfam; PF00047; ig; 1.
Pfam; PF00047; ig; 1.
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InterPro; IPR000742;
                       PIR; A47171; A47171.
HSSP; P00740; 1EDM.
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    MBL;
    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                        972 AAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAA----- 1025
                                                                                                                                                                                                      1083 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT 1142
                                                                306 GlyAlaValAspAspArgLysAlaSerGlyLeuAsn---GlyGluAlaSerArgSerGln 324
                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS VO AND V1).

SETRAIN=White ledjorn; TISSUE=Limb bud;

MEDLINE=93300846, PubMed=8314802;

Shinomura T., Nishida Y., Ito K., Kimata K.;

Shinomura T., Nishida Y., Ito K., Kimata K.;

Shinomura G. Marchada Y., Ito K., Kimata K.;

shinomura T., Nishida Y., Ito K.,

"cDNA cloning of PG-M, a large chondroit n sulfate proteoglycan

expressed during chondrogenesis in chick limb buds. Alternative,

spliced multiforms of FG-M and their relationships to versican.",

J. Biol. Chem. 268:14461-14469(1993)

-I FUNCTION: May play a role in intercellular signaling and in

connecting cells with the extracellular matrix. May take part in

the regulation of cell motility, growth and differentiation. Binds
                                                                                                                         ---GTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developing limb buds.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                                                                                                                                                                                                                         090953; 090945;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-1- SIMILARITY: Contains 2 link domains.
-1- SIMILARITY: Contains 2 ESF-like domains.
-1- SIMILARITY: Contains 1 C-type lectin family domain.
-1- SIMILARITY: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isold=Q90953-2; Sequence=VSP 003093;
TISSUE SPECIFICITY: Prechondrogenic condensation area of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hyaluronic acid.
SUBCELLULAR LOCATION: Secreted; extracellular matrix.
ALTERNATIVE PRODUCTS:
272 AlaSerLeu---LeuAlaLeuAlaLeuIleLeuAlaValCys-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q90953-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X60226; CAA42787.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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N-LINKED N-L	5	CHICK	AATCCGGATGT: : ::: AlaGlnGlnT	ACTCTCCATCC    GlnLeuL		cAspGlnThrV.	rgcrcrgaag      tGlyLysLysG	CATCTGGACCA	GAGCTTTCCATCCAGGTGTCATGCAGATT- 	SCTGAATTTCA	GGACCAAGTTG ::: [GlyAsnMetT	AGATGGATTCG        aAspGlySerV	GGGAAAATGGGGTGGGTGTCCTGATT     	ACAGTTTGCAG :     sPheAspA	F :: 7
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------GlySerHisSerThrLysGluProThrLysLysSerMetGluAlaLy 586
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648 GCAACACAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTAC 707
                                  374 LysValThrLeuLysProSerValPheGluSerSerValThrGluValAlaValThrLys 393
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467 aAlaLeuGluValGluHisThrTyrSerGluAla-GluLeuSerGluGluGlnGly----
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----SerValSerLeuThrLysGluAsnLeuTyrLeu----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).

DOMAIN: Two globular domains, G1 and G2, comprise the amino maken up the COOH terminus of the proteoglycan, while another globular region, G3, makes up the COOH terminus G1 contains link domains and thus consists of three disulfide-bonded loop structures designated as the A, B, C motifs. G2 is similar to G1. The keratan sulfate (KS) and the chondroitin sulfate (CS) attachment domains lie between G2 and G3.
                                                                                                                                                                                                                                                                                      MEDLINE=98209637; PubMed=9550267; Plannery C.R., Little C.B., Caterson B.; Plannery C.R., Little C.B., Caterson B.; Molecular cloning and sequence analysis of the aggrecan interglobular domain from porcine, equine, bowine and owine cartilage: comparison of proteinase-susceptible regions and sites of keratan sulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: Contains mostly chondroitin sulfate, but also keratan sulfate chains, N-linked and O-linked oligosaccharides (By similarity). SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: This proteoglyon is a major component of extracellular matrix of cartilagenous tissues. A major function of this protein is to resist compression in cartilage. It binds avidly to hyaluronic acid via an amino-terminal globular region. May play a regulatory role in the matrix assembly of the cartilage.
-i- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                              pig laryngeal cartilage.
                                             Chordata, Craniata, Vertebrata, Euteleostomi,
Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                           TISSUE=Cartilage;
MEDLINE=93038505; PubMed=1417734;
Barry F.P., Gaw J.U., Young C.N., Neame P.J.;
"Hyaluronan-binding region of aggrecan from pig laryngeal cart:
Amino acid sequence, analysis of N.linked oligosaccharides and
location of the keratan sulphate.";
Biochem. J. 286:761-769(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95128522; PubMed=7827755; Barry F.P., Neame P.J., Sasse J., Pearson D.; "Length variation in the keratan sulfate domain of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Proteoglycan; Repeat; Immunoglobulin domain.
NON TER 1 1 1 1 1 DOMĀIN 28 124 IG-LIKE V-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodom; PD000918; Link; 2.
PROSITE; PS01241; LINK; 2.
PROSITE; PS00615; C_TYPE_LECTIN 1; PROSITE; PS50041; C_TYPE_LECTIN_2; PROSITE; PS50835; IG_LINE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, S74664; AACC0528.2; -. PIR; S78009; S78009. InterPro; IPR001304; Lectin_C. InterPro; IPR000538; Link.
                                                                                                                                                                                                                                                                                                                                                                                       Matrix Biol. 16:507-511(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 14:323-328(1994),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF019757; AAC48799.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 454-537 FROM N.A.
                                                                                                                                                                                                                                                          SEQUENCE OF 324-453 FROM N.A.
                                                                                                                                                                                                                                                                          TISSUE=Chondrocytes;
                                               Eukaryota; Metazoa;
                                                              Mammalia; Eutheria;
 (CSPCP) (Fragments)
                                                                                                             1-370.
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Cartilage;
                                                                               NCB1_TaxID=9823;
                              scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                      substitution.
                                                                                                             SEQUENCE OF
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806
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                                                                                                                                                                                                                                                                                                                                                                                           GluLysPheThrPheGlnGluAlaAlaAsnGluCysArgArgLeuGlyAlaArgLeuAla 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TGGAAGGTT 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuAlaAspArgSerValArgTyrProlleSerLysAlaArgProAsn-----CysGly 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyasnLeuLeuGlyValArgThrValTyrLeuHisAlaAsnGlnThrGlyTyrProAsp 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluAsnPhePheGlyValGlyGlyGluGluAspIleThrIleGlnThrValThrTrpPro 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :::|||
363 AspValGluLeuProLeuProArgAsnIleThrGluGlyGluAlaArgGlyThrValIle 382
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(POTENTIAL).
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                     G1-A.
G1-B.
G1-B.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Matches:
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CS-1.
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N-LINKED
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N-LINKED
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26.36%
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252
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237
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DISULFID
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DOMAIN
CARBOHYD
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NON TER
SEQUENCE
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EMBL; JO44...

EMBL; M13933; AAA...

EMBL; M13933; AAA...

FIRSP; D80709; 1BF9.

R InterPro; IPR002353; Antifreezell.

DR InterPro; IPR00152; Asx.hydroxyl_S.

InterPro; IPR00181; EGF 2.

ThterPro; IPR001881; EGF 2.

ThterPro; IPR001881; EGF 7.
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InterPro; IPR001304; Lectin C.
InterPro; IPR001324; SGXXSG.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00108; EGF; 1.
Pfam; PF001047; ig; 1.
Pfam; PF001319; SGXXSG; 56.
Pfam; PF001319; SGXXSG; 56.
Pfam; PF001319; SGXXSG; 56.
Pfam; PF001319; SGXXSG; 56.
Pfam; PF001319; NINF; 4.
PRINTS; PR01326; LINKMODULE.
PRODOM; PF0010918; Link; 4.
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EMBL; S74657; AAC60751.1; -.
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EMBL; J04028; AAA48719.1; --
EMBL; M13993; AAA48720.1; --
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SMART; SM00034; CLECT; 1.
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    443 PheThrSerGluAspLeuValValGlnValThrSerAlaAlaThrGluGluGlyThrGlu 462
                         -----ACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAATAAA 851
                                              PGCA CHICK STANDARD; PRT; 2109 AA.
P07858; Q90810; Q90891; Q91047;
01-AUG-1988 (Rel. 08, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP).
                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89908500; PubMed=3170613;
Tanaka T., Har-El R., Tanzer M.L.;
"Partial structure of the gene for chicken cartilage proteoglycan
                                                                                                                                                                                                                                                                                                                    MEDLINE=94043149; PubMed=8226878;
Li H., Schwartz N.B., Vertel B.M.;
"cDNA cloning of chick cartilage chondroitin sulfate (aggrecan)
protein and identification of a stop codon in the aggrecan gene
associated with the chondrodystrophy, nanomelia.";
J. Biol. Chem. 268:23504-23511(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Cartilage;
MEDLINE=93111968; PubMed=1339285;
Chandrasekaran L., Tanzer M.L.;
"Molecular cloning of chicken aggrecan. Structural analyses.";
Biochem. J. 288:903-910(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primorac D., Stover M.L., Clark S.H., Rowe D.W.; "Molecular basis of nanomelia, a heritable chondrodystrophy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE 86259736; PubMed=3460082; Sai S., Tanaka T., Kosher R.A., Tanzer M.L.; "Cloning and sequence analysis of a partial cDNA for chicken cartilage proteoglycan core protein."; Proc. Natl. Acad. Sci. U.S.A. 83:5081-5085(1986).
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Biol. Chem. 263:15831-15835(1988).
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                                                                                                                                                                                                                                                                                                           STRAIN=White leghorn; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90307744; PubMed=1694853;
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Biochem. J. 296:885-887(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1042-1559 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matrix Biol. 14:297-305(1994).
                                                                                                                                                                                                                 Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=White leghorn;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo;
                         807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epitope."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate chains, N-linked and O-linked oligosaccharides.
-!- DISEASE: DERECTS IN AGC1 ARE THE CAUSE OF NANOMELIA, A LETHAL CONNECTIVE TISEASE: DERECTS IN AGC1 ARE THE CAUSE OF NANOMELIA, A LETHAL (CHONDROPYSTROPHY) CHARACTERIZED BY SHORTENED BAND MALFORMED LIMBS. AGGRECAN IS TRUNCATED AT ITS C-TERMINAL IN THE CS-2 BINDING DOMAIN AND IS NOT ANYONGE SECRETED FROM THE CHONDROCYTES.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 4 link domains.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isold=P07898-2; Sequence=VSP 003073; DOMAIN: Two globular domains, Gl and G2, comprise the amino terminus of the proteoglycan, while another globular region, G3, makes up the COOH terminus. Gl contains link domains and thus consists of three disulfide-bonded loop structures designated as the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS) and the chondroitin sulfate (CS) attachment domains lie between G2
                                    matrix of cartilagenous tissues. A major function of this protein
FUNCTION: This proteoglycan is a major component of extracellular
                                                                                        is to resist compression in cartilage. It binds avidly to hyaluzonic acid via an amino-terminal globular region. May play regulatory role in the matrix assembly of the cartilage. SUBCELLUIAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P07898-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                        similarity).
-!- ALTERNATIVE PRODUCTS:
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:::::: ||| |||||| ::: ||| GluLysPheThrPheGlnGluAlaPheAspLysGYsHisSerLeuGlyAlaArgLeuAla 277

258 390 278 450 298

6 6 6 6 6 6 6

330 CAGCAGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAAGGCTGCTGGGACTAAGTTTGGCC

449

503

504 AAAATGGGGTGGGTGTC---CTGATTTGGAAGGTTCCAGTG----

-----AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCG 596

LeuAlaAspArgSerValArgTyrProlleSerArgAlaArgProAsn-----CysGly 315

:::||| 354 LeuValProGlyLeuPheThrAspGluValGlyThrGluLeuGlySerAlaPheThrIle 373

597 TGCATTCCA------GAAATTATCACCACCAAAGATCCCATATTCAACAC 641

336

g

8 6 8 6

543

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R SMART; SM00179; EGF_CA; 1.

R SMART; SM00440; IG; 1.

SMART; SM00440; IG; 1.

R PROSITE; PS00010; ASX HYDROXYL; 1.

R PROSITE; PS00011; C_TYPE_LECTIN_1; 1.

R PROSITE; PS00021; EGF_1; 1.

R PROSITE; PS00026; EGF_3; 1.

R PROSITE; PS00187; EGF_CA; 1.

R PROSITE; PS00187; EGF_CA; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01241; LINK; 4.

Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain; Alternative splicing; Repeat; Immunoglobulin domain.
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LINK 2.
LINK 4.
LINK 4.
19 X 20 AA TANDEM-REPEAT.
EGFLIKE.
C-TYPE LECTIN.
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74
27
104
69
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G1-B.
G1-B.
G1-B.
G2-B.
C2-B.
KS.
CS-1.
CS-1.
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GTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCCTACTACT 731

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392 732 411 792

8 8 8 8

CAAACTGCAACACAACA

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GAAGTITTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAATAAA

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8 6 8 6 8 6

ACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATTTGTGTCACA

851

----ProArgGluGluAsn---

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454

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ACAGAATTTATT 671

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RESULT 13

TSG6_HUMAN

ID TSG6_HUMAN

AC P98066; QSWM19;

DT 01-FEB-1996 (Rel. 33, Created)

DT 15-MAR_2004 (Rel. 33, Last sequence update)

DT 15-MAR_2004 (Rel. 33, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annocation update)

DT 01-FEB-1996 (Rel. 33, Last annocation) update)

DT 01-FEB-1996 (Rel. 34). Last noncation update)

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DT 01-FEB-1996 (Rel. 34). Last annocation update)

CN TNFAIPFO OR TSG6.

OC NAMMALIA: Ruthan).

OC Mammalia: Eutheria; Craniata; Vertebrata; Euteleostomi;

OX NCBI TAXID=9606;

RN 11
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TISSUE=Fibroblast;
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JS-10-079-111-2 (1-2029) x PGCA\_CHICK (1-2109)

972 AAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAAGTAGTA 1031

460 SerGlyThrAlaPheThrThr-------GlyMetAlaGluValSerSerVal 474

912 GCTCTCCTCTTTGGTGCTGCTGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTG 971

----valThrThrServal

852 GCAGCATTCAAGAATGAAGCTGCTGGTTTTGGAGGTGTCCCCCACGGCTCTGCTAGTGCTT 911

---ValThrArgGluGluIleThrGlyIleTrpAlaValProGluGlu------

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                                                                                                                                                                                                                                                                                        TISSUENCE FROM N.A.

TISSUELELUNG, and Spleen;

MEDLINE=238825; Pubmed=12477932;

MEDLINE=238825; Pubmed=12477932;

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Applern M.S., Jordan H., Moore T., Max S.I., Wang J., Haib N.K., Applerno M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheerz T.E., Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheerz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Alakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Butkealey R.W., Touchman J.W., Scheuntz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Gnercth A., Schein J.E., Jones S.J.M., Marra M.A.; Proc. Natl A., Schein J.E., Jones S.J.M., Marra M.A.; Proc. Natl A., Schein J.E., Jones S.J.M., Marra M.A.; Proc. Natl A., Schein J.E., Jones S.J.M., Marra M.A.; Proc. Natl A., Schein J.E., Jones S.J.M., Marra M.A.; Proc. Natl A., Schein J.E., Jones S.J.M., Marra M.A.; Proc. Natl A., Schein J.E., Jones S.J.M., Marra M.A.; Proc. Natl A., Schein J.E., Jones S.J.M., Marra M.A.; Stolich D. Proc. Natl A., Schein J.E., Jones S.J.M., Marra M.A.; Schein J.E., Jones S.J.M., Marra M.A.; Schein J.E., Jones S.J.M., Abrama and mouse Colp. Sequences.";
MEDLINE=92112993; PubMed=1730767;
Lee T.H., Wisniewski H.-G., Vilcek J.;
A novel secretory tumor necrosis factor-inducible protein (TSG-6) is a member of the family of hyaluronate binding proteins, closely related to the adhesion receptor CD44.";
J. Cell Biol. 116:545-557(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANT GLN-144.
MEDLINE-21975206; bubMed=11854277.
Mentwich H.A., Mustafa Z., Rugg M.S., Marsden B.D., Cordell M.R.,
Mahoney D.J., Jenkins S.C., Dowling B., Fries E., Milner C.M.,
Loughlin J., Day A.J.;
"A novel allelic variant of the human TSG-6 gene encoding an amino
acid difference in the CUB module. Chromosomal localization,
frequency analysis, modeling, and expression.";
J. Biol. Chem. 277:15354-15362(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 600410; -. GO; GO:0004895; F:cell adhesion receptor activity; TAS. GO; GO:0005540; F:hyaluronic acid binding; TAS. GO; GO:0007267; P:cell-cell signaling; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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-!- SIMILARITY: Contains 1 link domain.
-!- SIMILARITY: Contains 1 CUB domain.
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EMBL, AJ421518; CAD13434.1; -.
EMBL, AJ419936, CAD12533.1; -.
EMBL, BC030205; AAH30205.1; -.
PIR, A41735; A41735.
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MIM; 600410; -.
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315 AGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAAGGCTACTG 374
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                                                                                                                                                                            TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6. LINK. CUB.
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BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

FT 2.

/FTIG=VAR_013005.
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PROSITE; PS01241; LINK; 1.
Cell adhesion; Signal; Glycoprotein; Polymorphism; 3D-structure.
SIGNAL 1 19 POTENTIAL.
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Matches:
Conservative:
Mismatches:
Indels:
GO; GO:0006954; P:inflammatory response; TAS. GO; GO:0007165; P:signal transduction; TAS.
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                                              Pfam; PF00431; CUB; 1.
Pfam; PF00193; Xlink; 1.
ProDom; P0000918; Link; 1.
SMART; SM0042; CUB; 1.
SWART; SM00445; LINK; 1.
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InterPro; IPR000538; Link.
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315 AGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTG 374
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MEDLINE=89380219; PubMed=2528543;
Antonsson P., Heinegaard D., Oldberg A.;
The keratan sulfate-enriched region of bovine cartilage proteoglycan consists of a consecutively repeated hexapeptide motif.";
J. Biol. Chem. 264:16170-16173(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGCA BOVIN STANDARD; PRT; 2364 AA.
P13608; P79117; Q28159;
01-JAN-1990 (Rel. 13, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP).
                                                                                                                                                                                                         GlyGlyArgLeuAlaThrTyrLysGlnLeuGluAlaAlaArgLysIleGlyPheHisVal
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BEDILINE-85027710; PubMed-6489519;
Perin J.-P., Bonnet F., Jolles J., Jolles P.;

Sequence data concerning the protein core of the cartilage
"Sequence data concerning the protein core of the satisfied of a sequence allowing the synthesis an oligomucleotide probe.";

FERS Lett. 176:37-42(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1609-2113 AND 2151-2364 FROM N.A.
MEDLINE=87270630; PubMed=3111460;
Oldberg A., Antonsson P., Heinegaard D.;
"The partial amino acid sequence of bovine cartilage proteoglycan, deduced from a cDNA clone, contains numerous Ser-Gly sequences arranged in homologous repeats.";
Biochem. J. 243:255-259(1987).
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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PubMed=8349621;
Fueloep C., Walcz E., Valyon M., Glant T.T.;
"Expression of alternatively spliced epidermal growth factor-like
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Hering T.M., Kollar J., Huynh T.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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Biol. Chem. 268:17377-17383(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                      375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Coding sequence, exon-intron structure and chromosomal localization of wurine TNF-stimulated gene 6 that is specifically expressed by expanding cumulus cell-ocyte complexes."; Gene 202:95-102[1997].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
-!- DEVELOPMENTAL STAGE: Expressed in cumulus cell-oocyte complexes
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
STRAIN=CD-1; TISSUB=Cumulus cell, Embryo, and Oocyte;
MEDLINE=98037423; PubMed=9427551;
Fueloep C., Kamalh R.V., Li Y., Otto J.M., Salustri A., Olsen B.R.,
Glant T.T., Hascall V.C.;
                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
M-1 ICD24722826088F9 CRC64;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
17-OCT-2003 (Fel. 42, Last annotation update)
18 timulated gene 6 protein)
18 timulated gene 6 protein)
18 TIMFAIP6 OR TAFIP6 OR TSG6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: Possibly involved in cell-cell and cell-matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interactions during inflammation and tumorgenesis (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         during expansion in vivo.
-!- SIMILARITY: Contains 1 link domain.
-!- SIMILARITY: Contains 1 CUB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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SMART; SMO0445; LINK; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01241; LINK; 1.
CEll adhesion; Signal; Glycoprotein.
SIGNAL.
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ProDom; PD000918; Link; 1.
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MGD; MGI:1195266; Tnfaip6.
InterPro; IPR000859; CUB.
InterPro; IPR000538; Link.
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Pfam; PF00193; Xlink; 1
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[9]

US-10-079-111-2 (1-2029) x TSG6\_MOUSE (1-275)

Query Match:

DOMAIN DISULFID DISULFID DISULFID

DOMAIN CHAIN

DISULFID CARBOHYD SEQUENCE

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Query Match:
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                                                                                                                                                                                                                                                                                            IsoId=P13608-2; Sequence=VSP 003072; DOMAIN: Two globular domains, Gl and G2, comprise the amino terminus of the proteoglycan, while another globular region, G3, makes up the C-terminus. Gl contains link domains and thus consists of three disulfide-bonded loop structures designated as the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS) and the chondroitin sulfate (CS) attachment domains lie between G2
                                                           PEBS Lett. 206:73-77(1986).

FEBS Lett. 206:73-77(1986).

-! FWOTION: This proteoglycan is a major component of extracellular larger. This proteoglycan is a matrix of cartilagenous tissues. A major function of this protein is to resist compression in cartilage. It binds avidly to hyaluronic acid via an amino-terminal globular region. May play a regulatory role in the matrix assembly of the cartilage.

-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                                                                                                                                                                                                                                                                        -!- TINKED (ABOUT 40) OLIGOSACCHARIDES.
-!- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND OLIGOSACCHARIDES.
-!- PTM: THE KERATAN SULFATE CONTENTS DIFFER CONSIDERABLY BETWEEN ADULT AND FETAL BOVINE PROTEOGLYCANS.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
PARTIAL SEQUENCE.
MEDLINE=87005253; PubMed=3530809;
Perin J.P., Bonnet F., Jolles P.;
"Structural relationship between link proteins and proteoglycan
                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                               IsoId=P13608-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: U76615; AAB38524.1; --
EMBL; U76615; AAB38524.1; --
EMBL; L07053; -; NOT_ANNOTATED_CDS.
PIR; T42630; T42630.
HSSP; P08709; 18F9.
INTERPO: IPR001253; AALIÉTEEZEII.
INTERPO: IPR001525; ASK_bydroxyl_S.
INTERPO: IPR00142; EGF_2.
INTERPO: IPR001881; EGF_2.
INTERPO: IPR001881; EGF_CA.
INTERPO: IPR00110; IG-IIke.
INTERPO: IPR003006; IG-IIke.
INTERPO: IPR003006; IG-IIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000538; Link.
InterPro; IPR003324; SGXXSG.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00356; ANTIFREEZEII.
PRINTS; PR01265; LINKMODULE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00059; lectin c; 1.
Pfam; PF02339; SGXXSG; 61.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probom; PD000918; Link; 4. SMART; SM00032; CCP; 1. SMART; SM00034; CLECT; 1. SMART; SM00179; EGF_CA; 1.
                                                                                                                                                                                                similarity).
ALTERNATIVE PRODUCTS:
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Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                Name=2
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330 CAGCAGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGCGGACTAAGTTTGGCC 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 LeuAlaAspArgSerValArgTyrProlleSerLysAlaArgProAsn-----CysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --TGGAAGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 GGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGGCTTTGAAACTTGCAGCTATGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 ThrThrGlyGlnLeuTyrLeuAlaTrpGlnGlyGlyMetAspMetCysSerAlaGlyTrp
                                                                                                                                                                                                                                                                                                                                                                                                        QF
                                                                                                                                                                                                                Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF-LIKE, CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                      AA APPROXIMATE TANDEM REPEATS
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(POTENTIAL).
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(POTENTIAL).
                                                                                                                                                                                                                                   splicing; Repeat; Immunoglobulin domain.
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...) (PO.
...NAC. ..) (POTA.
...) (GLCNAC. ..) (POTFY.
q (in isoform 2).
?P 003072.
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W; 6FF83763420C3D4C CRC64;
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46
                                                                                                                                                                                                                                                     POTENTIAL.
AGGRECAN CORE PROTEIN.
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Mismatches:
Indels:
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N-LINKED (GLCNAC.
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E-[EK]-P-F-P-S.
CS-2.
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Matches:
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SUSHI
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SMART; SM00445; LINK; 4.
PROSITE; PRO0610; ASX HYDROXYL; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS01187; EGF_Z; 1.
PROSITE; PS01187; EGF_ZA; 1.
PROSITE; PS00290; IG MAC; FALSE_NEG.
PROSITE; PS01241; LINK; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504 AAAATGGGGTGGGTGTCCTGATT-----
                                                                                                                                                                                                                                                                                                                                                            LINK 3.
LINK 4.
                                                                                                                                                                                                                                                                                                                     LINK 1
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||| :::||||||| 320 GlyAsnLeuLeuGlyValArgThrValTyrLeuHisAlaAsnGlnThrGlyTyrProAsp 339
                                                                                         356
                                                                                                                       597 TGCATTCCAGAA-----ATTATCACACC 620
                                                                                                                                                 621 AAAGATCCCATATTCAACACTCAAACTGCAACAACAACAAGAATTTATTGTCAGTGAC 680
                                                                                                                                                                                                                              376 ThrTrpProAspValGluLeuProLeuProArgAsnIleThrGluGlyGluAlaArgGly 395
                                                                                                                                                                                                                                                                  681 AGTACCTACTCGGTGGCATCCCCTTACTCTACATACCTGCCCCTACTACTACTCCTCCT 740
                                                                                                                                                                                                                                                                                          ||| ||| ||| ||| 396 SerVallleLeuThrAlaLysProAspPheGluVal---SerProThrAlaProGluPro 414
                                                                                                                                                                                                                                                                                                                                                             ||| :::||| | ::||| 415 GluGluProPheThrPheValProGluValArg-------AlaThrAlaPhe 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            537 CCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCG 596
                                                                                                                                                                                                                                                                                                                                         741 GCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATTTGTGTCACAGAAGTTTTT 800
                                                                                                                                                                                                                                                                                                                                                                                                              801 ATGGAAACTAGCACCATGTCTACAGAA---ACTGAACCATTTGTTGAAAATAAAGCAGCA 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----Ala 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CTG 902
                                                                            ||| ||||| ::: |||||| 340 ProSerSerArg---TyrAspAlaIleCysTyrThrGlyGluAspheValAsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                        430 ProGluValGluAsnArgThrGluGluAlaThrArgProTrp----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 858 TICAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCT----
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465 ValValGlnValThrLeuAlaProGlyAlaAla 475
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Search completed: September 13, 2004, 10:22:55 Job time : 63.5 secs

score:

Title: Perfect

Run on:

Sequence:

Scoring table:

Minimum DB Maximum DB

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No. Result

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Q9W684 gallus gall
Q8M694 homo sapien
Q80537 mus musculu
Q80544 homo sapien
Q92493 homo sapien
Q91533 homo sapien
Q91533 homo sapien
Q81647 gallus gall
Q8K0K6 mus musculu
Q87474 mus musculu
Q9449 homo sapien
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Q90zl8 anas platyr
Q9H5a5 homo sapien
Q96j24 homo sapien
Q96za7 homo sapien
Q86z27 homo sapien
Q86r22 homo sapien
Q86r72 homo sapien
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Q62913 rattus norv
Q9h7h7 homo sapien
Q86ur4 homo sapien
                      Q8bhc0 mus musculu
                                 Q99ne4 mus musculu
                                           Q7ys22 sus scrofa
008779 rattus norv
070509 rattus norv
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Q8wwq8 homo sapien
                                                                        Q9uj36 homo sapien
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"HAR: a novel homolog of CD44 and putative hyaluronic acid receptor
encoded by a gene on human chromosome 11p15.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF127670; AAD49220.2;
HSSP; P98066; 1TSG.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
INTERPRO; IPRO00538; Link.
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Q9H5A6
Q9H5A3
P79787
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Q8BM87
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Q9H7H7
Q8TC18
Q9Y5Y7
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01-MAX-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
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-MODEL=frame+ n2p:model -DEV=xlp
-MODEL=frame+ n2p:model -DEV=xlp
-G=/cgn2_1/USFYC_spool p/US10079111/runat_13092004_102126_1826/app_query.fasta_1.2183
-G=/cgn2_1/USFYC_spool p/US10079111/runat_13092004_102126_1826/app_query.fasta_1.2183
-DBSPTREMBL_25 -QFMM=fastan -SUFFIX=rspt -MINMATCH=0.1 -LGOPCL=0 -LGOPEXX=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UOCALIGN=200 -TRR_SCORE=pct -TRR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcc -NORM=ext -HEAFSIZE=560 -MINIEN=0 -MAXIEN=2000000000
-USER=US10079111 @CGN 1 1 344 @runat_13092004_102126_1826 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGS_SCORES=0 -MAXIT -DSPBADCK=100 -LONGING
-DBV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPPP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                       using frame_plus_n2p model
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Listing first 45 summaries
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SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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                                                                                                LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLyr
              AAAGTAGTAAAAGGAGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P SEQUENCE FROM N.A.
TISSUB-Liver;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOGES131, AAH26231.1;
EMBL; BCOGES131, AAH26231.1;
GO; GO: 0005540; F: hyaluronic acid binding; IEA.
R Go; GO: 0005540; F: hyaluronic acid binding; IEA.
R GO; GO: 0005581; F: hyaluronic acid binding; IEA.
R GO; GO: 0005581; Link:
R InterPro; IPR00193; Link:
R Prodom; PD00198; Link; 1.
R PRINTS; PR01265; LINK: 1.
SMART; SM00445; LINK; 1.
C SEQUENCE 322 AA; 35183 MW; OBIEDBD76CE4610A CRC64;
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Best Local Similarity: 9
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                                     ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeulle
                                                                                                                                                                                                                                                                                                                                                                  GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCCCACGGCTCTG
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                                                                                                                                                                                                                             CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT
                                                                                                                                                                                                                                                                                               TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Lymphatic endothelium-specific hyaluronan receptor LYVE-1.
Homo sapiens (Human).
Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Eutelec Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
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ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                       21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArg1leMetGly
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Matches:
Conservative:
Mismatches:
Indels:
wounding;
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|SerTyrGlyTrpValGlyGluGlnPheSerValIleProArgllePheSerAsnProArg 104
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LeuThrLeuAlaSerArgAspGlnValGluSerAlaGlnLysSerGlyPheGluThrCys
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ArgasnLysasnProGlnMetAsnPheThrGluAlaAsnGluAlaCysLysMetLeuGly
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182 ArgalaProProLeuThrSerMetAlaArgLysThrLysLysIleCysIleThrGluVal
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinga; Musingal_TaxID=10090;
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01-07N-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Mus musculus (Mouse)
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LeuValGlnAspLeuSerIleSer---ThrCysArglleMetGlyValAlaLeuValGly 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CSTBL/6J; TISSUE=Lung; MEDLINE=2235681; PubMed=1246681; The REANTOW CONSORTIUM; The PANTOW CONSORTIUM; The RIKEN Genome Exploration Research Group Phase I & II Team; Hanalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                    GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT
                                 AAAGTAGTAAAGGAGGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg K.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC038653; AAH38653.1; --
EMBL; BC038892; AAH38892.1; --
EMBL; AK004726; BAC25094.1; --
EMBL; MGI:2136348; Xikd1.
GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:0005886; F:transmembrane receptor activity; IDA.
GO; GO:0006027; F:transmembrane receptor activity; IDA.
GO; GO:0006027; F:transmembrane receptor activity; IDA.
GO; GO:0006027; F:diamsmembrane receptor activity; IDA.
GO; GO:0006027; F:diamsmembrane receptor activity; IDA.
GO; GO:0006027; F:diamsmembrane receptor activity; IDA.
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221
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CZECH II; TISSUE-Lung, and Mammary gland;
                                                                                                                                                                                                                                                                      318 AA
                                                                                                                                                                                                                                                                                               UL-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequenc
01-OCT-2003 (TrEMBLrel. 25, Last annotat
Extra cellular link domain-containing 1.
XLKD1.
Mus musculus (Mouse).
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79.18%
69.72%
30.60%
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ProDom, PD000918; Link, 1.
SMART; SM00445; Link; 1.
PROSITE; PS01241; LINK: 1
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318 AA; 34573
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                                                                STRAIN-Balb/c, TISSUE-Digestive tract;

XX MEDLINE=21276443; PubMed=11278811;

Prevo R., Banerij S., Ferguson D.J.P., Clasper S., Jackson D.G.;

Prevo R., Banerij S., Ferguson D.J.P., Clasper S., Jackson D.G.;

Mouse LYVE-1 is an endocytic receptor for hyaluronan in lymphatic

T. J. Biol. Chem. 276:19420-19430(2001).

EMBL; A3311501; CA33082.1; -.

RBBL; A3311501; CA33082.1; -.

RBBL; A3311501; CA33082.1; -.

RBC; GO:0005846; XIAG.

GO:0005846; XIAG.

RO; GO:0005846; XIAG.

RO; GO:0006886; C:plasma membrane; IDA.

RO; GO:0006887; F:transmembrane receptor activity; IDA.

RO; GO:0006027; P:glycosaminoglycan catabolism; IDA.

InterPro; IPR00193; Link; 1.

RP ProDom; PD000918; Link; 1.

RP ProDom; PD000918; Link; 1.

RP PROSITE: PS01241; LINK; 1.
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MEDLINE=99156989; PubMed=10037799; Banerji S.; "LYVE-1, a new homologue of the CD44 glycoprotein is a lymph-specific receptor for hyaluronan."; J. Cell Biol. 144:789-801(1999).
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318 LY
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                                                                                                                   PheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeuLeuValLeuAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                 262 PheProPheThrThrLysAsnGlnGlnLysGluMetIleGluThrLysValValLysGlu
738 CCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTCACAGAAGTT
                          |||||||
182 ArgalaProProLeuThrSerMetAlaArgLysThrLysLysIleCysIleThrGluVal
                                                                                           TTTATGGAAACTAGCACCATGTCTACAGAAACTGAAACCATTTGTTGAAAATAAAGCAGCA
                                                                                                                                                                                    CTCTTCTTTGGTGCTGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCC
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Lymphatic endothelial hyaluronan receptor LYVE-1 (Fragment).
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Michael K.W., Xu S.-H., Voisine P., Khan T.A., Feng J.,
Sellke F.W., Blanchi C.;
"Identification of pig LYVE-1.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY304537; AAP69946.1; -
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
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Score: 138  Percent Similarity: 34.29\$ Conservative: 77  Best Local Similarity: 22.01\$ Mismatches: 254  Query Match: 11 Gaps: 160  DB: 11 (1-2029) x 008779 (1-780)	Qy 225 IGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCA	Qy 285 TCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGGGAACCAGCAGCTGAATTTC 344	Qy 345 ACAGAAGCTAAGGAGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTT 404	Qy 405 GAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGGCTGGGTTGGAGATTC 464	Qy 465 GTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGGGAAAAATGGGGTGGGT	Qy 525 ATTIGGAAGGITCCAGIGAGCCGACAGITIGCAGCCTATIGITACAACTCAICIGATACT 584	Qy 585 TGGACTAACTCGAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAA 644	Oy 645 ACTGCAACACAACAGAATTTATTGTCAGTGACAGTGCTACTCGGTGGCATCC 701  Db 144 AspGlyProValThrlleThrlleValAsnArdAspGlyDhrArdTyrSerLysIvsGly 163	702 CCTACTCTACAATACCTGCCCCTACTACTACTCCTCCTGCTCCAGGT	Qy 750 TCCACTTCTATTCCACGGAGAAAAATTGATTTGTGTCACAGAAGTTTTTATGGAAACT 809	Qy 810 AGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGAA 869	870 GCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGCT	210 GCTGCAGCTGGTTTTTGCTATGTAAAAGGTATGTGAAAAGGCTTTCCCT 98	229	Qy 984TTTACAAACAAGAATCAGCAGAAATGAATGAACCAAA 1025	1026 GTAGTAAAGGAGAGAAGGCCAATGATAGCAACCCTAATGAGAATCAAAGAAAACTGAT :::	261 ThrThrThrAlaThrThrAlaLeuMe	AlaginAsnTroPheSetTroPhePheGlnProSerGluSerLysSerHisleulisTh	1122 ACCGTGCG-ATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACCTGA 1
Oy 543 AGCGACAGTTTGCAGCCTATTGTTACAACTCGATACTTGGACTTACTGGGATT 602	Oy 663 GAATTTATTGTCAGTGCGTCTACTCGGTGGCATCCCCTTACTCTACAATA 716	Qy 717CCTGCCCCTACTACTACTCCTCCTGCTCCACTTCTATTCCACGGAGAAAA 773	Qy 774 AAAITGATTIGIGCACAGAAGITITITAIGGAAACIAGCACCAIGICTACAGAAACIGAA 833	Qy 834 CCATTIGITGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGTCCC 893  141 LeuTyrileGluAsnArgThrAlaPheLysAsnGluAlaIleGlyPheGlyGlyIlePro 160	Qy 894 ACGGCTCTGCTTGCTCTCTTCTTTGGTGCTGCAGCTCTTGGATTTTGC 953	Qy     954 TAIGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAACAAGAATCAGCAGAAATG 1013       Db     181 TyrvallysArgTyrvallysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMet 200	Qy 1014 ATC 1016 	RESULT 7 008779 ID 008779 PRELIMINARY: PRT: 780 AA.	(TrEMBLrel. 04, Created) (TrEMBLrel. 04, Last sequence (TrEMBLrel. 25, Last annotati	CD44 protein. CD44. Rattus norvegicus (Rat). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,			EMBL; U96138; AAB5402.1; EMBL; GELINALIN, DUDU GREGORGE HSSP. P98066; ITSG.		DR GO; GO: 00037155; P: Cell adhesion; IEA. DR InterPro; IPR001231; CD4 antigen. DR InterPro; IPR000538; Link.		DR ProDom; PD000918; Link; 1. DR SMART; SMO0445; LINK; 1. DB DD047TF; D800131; TNK: 1	SEQUENCE	Alignment Scores: Pred. No.: 1.26e-13 Length: 780

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184 SerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThrAspLeuPro 203
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30 ThrCysArgTyrAlaGlyvalPheHisValGluLysAsnGlyArgTyrSerIleSerArg 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 GTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGTGTCCTG
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           Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                Stevens J.W.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                  GO; GO: 001622; C: membrane; IEA.
GO; GO: 0016895; F: cell adhesion receptor activity; IEA.
GO; GO: 000540; F: Pyaluronic acid binding; IEA.
GO; GO: 0005540; F: Pyaluronic acid binding; IEA.
GO; GO: 001515; P: cell adhesion; IEA.
InterPro; IPR001231; CD44 antigen.
InterPro; IPR001538; Link.
PRINTS; PR01265; LINKMODULE.
PRINTS; PR01265; LINKMODULE.
PROD0918; Link; 1.
SMART; SM00445; LINK; 1.
PROSITE; PR01241; LINK; 1.
PROSITE; PR01241; LINK; 1.
SEQUENCE 364 AA; 39725 MW; BA249776C4419AA7 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                   STRAIN=Sprague-Dawley; TISSUE=Lumbar spine;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glycoprotein CD44s.
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    555 GCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------LeuMetSerThrSerAlaThrAlaThrGluThr
 C319E5CE5C0B51D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 AspSerThrAspArgIleProAlaThrThr-------
                                                     742
1117
63
175
203
                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AlaThrLysArgGlnGluAla--TrpAspTrp
                                                                                                                       Indels:
                                                                                                                                       Gaps:
                                                                                                                                                                         US-10-079-111-2 (1-2029) x Q9UJ36 (1-742)
 742 AA; 81598 MW;
                                              4.39e-13
226.00
32.26%
20.97%
6.27%
                                                                                                     Best Local Similarity:
                                                                                     Percent Similarity:
                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                              |||::::||||:::|||298 CysGlyGlnLysLysLysLeuVallleAsnSerGlyAsnGlyThrValGluAspArgLys 317
                                                                                        318 ProSerGluLeuAsn---GlyGluAlaSerLysSerGlnGluMetValHisLeuValAsn 336
                       --AAT 866
                                                                                                                                       887
                                                                                                                                                                       GluLeuAlaGlyHisSerSerGlyAsnGlnAspSerGlyValThrThrThrSerGlyPro 263
                                                                                                                                                                                                                                                                          GCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAAC 992
                                                                                                                                                                                                                                                                                                            ----IleAlaValAsnSerArgArg 297
CGGAGAAAAAATTGATTTGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACA 824
                                                                                                                                                                                                         --- GICCCCACGCTCTGCTAGTGCTTGCTCTCCTCTTTGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gunthert U.;
"CD44: a multitude of isoforms with diverse functions.";
"CD4: a multitude of isoforms with diverse functions.";
Curr. Top. Microbiol. Immunol. 184:47-63(1993).
EMBL; AJZ51595; CZB61878.1; -.
PIR; A47195; A47195.
HSSP; P98066; ITSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCTGAA 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gunthert U.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
TRANSMEMBRANE GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| |||::::::|||
LysGluProThrGluThrProAspGlnPheMetThrAlaAsp 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Most Group of Thembrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004895; F:cell adhesion receptor activity; IEA.

GO; GO:0005540; F:hyaluronic acid binding; IEA.

GO; GO:0007155; P:cell adhesion; IEA.

InterPro; IPR001211; CD44 antigen.

InterPro; IPR000538; Link.
                                                                   ---GAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane glycoprotein precursor.
                                                                                                                                       GAAGCTGCTGGGTTTGGAGGT----
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MEDLINE=94147793; PubMed=7508842;
                                                                                                                                                                                                                                                                                                         AlaLeuIleLeuAlaValCys-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; Provides, CD44.
PRINTS; PROGGS8; CD44.
PRINTS; PRO1265; LINKWODULE.
ProDom; PD000918; Link; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01241; LINK; 1
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                                                                                                                                                                                                         Homo sapiens (Human)
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SIGNAL
CHAIN
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105 TyrLysLeuSerAlaAsnThrThrGlyArgTyrAspAlaTyrCysTyrAsnAlaThrGlu 124
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| GlyGluIleValIlleAspAsnGluAspGlySerArgTyrAsnAlaAspGlyThrArgHis 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             648 GCAACACAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTAC 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||
| hrargasplysalaCysGluProlleGluArglleAspThrSerPheLeuSerAsnGln
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6 ValTrpAlaThrPheGlyLeuCysLeuLysLeuCysLeuThrGluThrGlnPheAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 GTGTCATGCAGAATTATGGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 ValSerCysArgTyrArgGlyValPheHisValGluLysAsnGlyArgTyrSerLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTGAAACAGCCTTGAAAGCTTAGAAACTTGCAGCTATGGCTGGGTTGGAGATGGA
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                                                                                                                                                                                                                                   77C176E0A898D081 CRC64;
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GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR001231; CD44 antigen.
InterPro; IPR001231; CD44
InterPro;
IPR00538; Link.
Pfam; PP00193; Xlink; 1.
PRINTS; PR006689; CD44.
PRINTS; PR001265; LINK, 1.
PRODOM; PD000918; Link; 1.
PROSITE; PS01241; LINK; 1.
PROSITE; PS01241; LINK; 1.
SEQUENCE 265 AA; 29215 MW; 77C176E0
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219.00
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Best Local Similarity:
                                                                                                                                                                                                                                                                                        Alignment Scores:
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Q90ZL8;
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ID Q90ZL
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                                                                                                                                                                                   ----ACTGATAAAACCCAGAAGAG 1100
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                                                                                  -1079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1452 ACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG 1511
                                                                                                                                                                                                                                                                                     1101 TCCAAGAGTCCAAGC-----AAAACTACCGTGCGATGCCTGGAAGCTGAAGTTTAG 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                              360
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     312 ProArgAlaPheAspHisThrLysGlnAsnGlnAspTrpThrGlnTrpAsnProSerHis 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --ProbeulleHisHisGluHisHisGluGluGluGluThr 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408 TrpHisGlu-----GlyTyrArgGlnThr------ProArgGluAspSerHisSer 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 ThrThrGlyThrAlaAlaAlaSerAlaHisThrSerHisProMetGlnGlyArgThrThr 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :::||| :::|||| ::---ThrSer-----
                                                                                                                                PheSerGlySerGlyIleAspAspAspGluAspPheIleSerSerThrIleSerThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
NCBI_TaxID=8839;
                                                                                                                                                                                                                                                                                                                   ||| :::|||
332 Ser---AsnProGluValLeuLeuGlnThrThrThrArgMetThrAspValAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                           -----ArgAsnGlyThrThrAlaTyrGluGlyAsnTrpAsn----
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STRAIN=White Pekin;
Chan S.W.S., Warr G.W., Middleton D.L., Higgins D.A.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF832869; AAK18277.1; -.
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GO; GO:0004895; F:cell adhesion receptor activity; IEA.
GO; GO:0005540; F:hyaluronic acid binding; IEA.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 15, Last annotation update)
T cell antigen CD44 isoform b.
Anas platyrhynchos (Domestic duck)
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165 SerGlyAspSerSerThrSerGlyValAspAspGluAsnValGlySerGlySerSerHis 184
                             TCTACAATACCTGCCCCTACTACT
                                                                                                                01-MAR-2001 (TrEMBLrel. 16, C. 01-MAR-2001 (TrEMBLrel. 16, Le 01-0CT-2003 (TrEMBLrel. 25, La DJ68D18.2.3 (CD44 antital system).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            719 AA; 78854 MW;
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                                                                                                       PRELIMINARY;
                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                system)) (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GITGAAACAGCCITGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGA 461
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145 GlyGluIleVallleAspAsnGluAspClySerArgTyrAsnAlaAspGlyThrArgHis 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 TyrLysLeuSerAlaAsnThrThrGlyArgTyrAspAlaTyrCysTyrAsnAlaThrGlu 124
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ValTrpAlaThrPheGlyLeuCysLeuLysLeuCysLeuThrGluThrGlnPheAsn
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 19, Last annotation update)
T cell antigen CD44 isoform a.
Anas platyrhynchos (Domestic duck).
Butaryota; Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
                                                                                                                       STRAIN=White Pekin;
Chan S.W.S., Middleton D.L., Warr G.W., Higgins D.A.;
"Anas placyrhynchos T cell antigens.";
Submitted (APR-2010) to the EMBL/GenBank/DDBJ databases.
EMBL; AY029553; AAK40246.1; -..
GO; GO:0004895; F:cell adhesion receptor activity; IEA.
GO; GO:0005540; F:hyaluronic acid binding; IEA.
GO; GO:000155; P:cell adhesion; IEA.
R GO; GO:00155; P:cell adhesion; IEA.
R InterPro; IPR001231; CD44_antigen.
R InterPro; IPR000538; Link.
R Pfam; PF00193; Xlink; 1.
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PRINTS; PR01265; LINKMODULE.
ProDom; PD000918; Link; 1.
SMART; SM00445; LINK; 1.
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SEQUENCE 398 AA; 43673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 CTGAATTTCACAGAAGCTAAAGGAGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG 395
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LeuAsnIleThrCysArgPheAlaGlyValPheHisValGluLysAsnGlyArgTyrSer 20
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21 IleSerArgThrGluAlaAlaAspLeuCysLysAlaPheAsnSerThrLeuProThrMet
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                                                                                                                                                                                                     (TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
(CD44 antigen (Homing function and indian blood group
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cobley V.;
Cobley V.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL133330, CAC10347.1;
EMBL; AL133310, CAC10347.1;
EMBL; AL133310, CAC10347.1;
CG; GC: 0004695; F: cell adhesion receptor activity; IEA.
GG; GC: 00005540; F: Envaluance; IEA.
RG; GC: 00005540; F: Envaluance; IEA.
RG; GC: 0000515; P: cell adhesion, IEA.
RINTERPO; IPR001231; CD44, antigen.
RINTERPO; IPR001638; Link; 1.
RRINTS; PR00193; Xlink; 1.
RRINTS; PR00194; LINK; 1.
RRINTS; PR00445; LINK; 1.
RRINTS; PR00445; LINK; 1.
RR PROSITE; PS0144; LINK; 1.
RR PROSITE; PS0144; LINK; 1.
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Matches:
Conservative:
Mismatches:
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185 AspThrThrProValAspThrSer 192
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                                                                                                                                                                            Created)
                                                                                                                   PRT;
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AlaPheAspGly 118	197 203 806 203 866 91 216 926 926 927 221 986 RRP 236 RRP 1046 RRP 987 887 986 RRP 986 RRP 986 RRP 986 RRP 986 RRP 986 RRP 986 RRP 986 RRP 986 RRP 986 RRP 986 RRP 986 RRP	1079 275 1079 295 1115 314	329 Pred. No.: 1232 Pered. No.: 500 Pered. No.: 1232 Percent Simila Best Local Sir Devent Match: DB: US-10-079-111- 342 Qy 255	
Seralaproprogludiua	178 ValHisProlleProAspGluAspSerProTrplleThrAspSerThrAspArgllePro 747 GCTTCCACTTCTATTCCACGGAGAAAAATTGATTGTGTCACAGAGATTTTATGGAA 198 AlaThrThr—————————————————————————————————	LeuSerPhese ThrThrProAr GAAGATCCAA SerHisSer		
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GGAGCTCAGACCCTTTCTTCACCTCTGAAA 1592
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serHisSerThrThrGlyThrAlaAlaAla 406
                                                                                TGACATGTCCTTCTGAGCCCGGTAAGAGC 1640
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krgThrThrProSerProGluAspSerSer 426
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tion update)
1 and indian blood group
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 ATCCAGGTGTCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGCAG 335
                                                                                                                                                1515 GITGAAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACC
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| LeuAsnIleThrCysArgPheAlaGlyValPheHisValGluLysAsnGlyArgTyrSer
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21 IleSerArgThrGluAlaAlaAspLeuCysLysAlaPheAsnSerThrLeuProThrMet
                                                              1455 TAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGG
                                                                                      CTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DJ68D18.2.4 (CD44 antigen (Homing function and indian blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cobley V.;

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. BMBL; AL133330, CAC10345.1;

EMBL; AL13330, CAC10345.1;

EMBL; AL13330, CAC10345.1;

EMBL; AL13330, CAC10345.1;

GO; GO:0016020; C:membrane; IEA.

GO; GO:000540; F:neal adhesion receptor activity; IEA.

GO; GO:0005540; F:hyaluronic acid binding; IEA.

R GO; GO:0007155; P:cell adhesion; IEA.

ENTOTES PRO0133; Link; I.

EMENTY: PRO0193; Link; I.

R PRINTS: PRO1265; Link, I.

R PRINTS: PRO1265; Link, I.

R PRINTS: PRO0658; Link; I.

R PRINTS: PRO0658; Link; I.

R SMART; SM00445; LINK; I.
                                                                                                                                                                                                                                                                                                                    TCTGAGCCCGGTAAGAGCAAAAGAATGGCAGAAAAGTTTAGCCCC 1667
                                                                                                                                                                                                                                                                                                                                            122C7250B7DA0F47 CRC64;
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104
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                                                                                                                                                                                                                                  1575 CTTTCTTCAGCTCTGAAAGAGAACACGTATCCCAC-----
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Mismatches:
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SEQUENCE 676 AA; 73929
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Best Local Similarity:
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                                                                                  495 AAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTT 554
                                                                                                                       96 IleCysAlaAlaAsnAsnThrGlyValTyrileLeuThrSerAsnThrSer---GlnTyr 114
                                                                                                                                                                                          ||||||||:::||||:
115 AspThrTyrCysPheAsnAlaSerAlaProProGluGluAspCysThrSerValThrAsp 134
                                                                                                                                                                                                                                                                                              135 LeuProAsnAlaPheAspGlyProIleThrIleThrIleValAsnArgAspGlyThrArg 154
                                                                                                                                                                                                                                                                                                                                          ------CCAGAAATTATCACCAAAGATCCCATA 632
                                                                                                                                                                                                                                                                                                                                                                                155 TyrValGlnLysGlyGluTyrArgThrAsnProGluAspileTyrProSerAsnProThr 174
                                                                                                                                                                                                                                                                                                                                                                                                                          633 ITCAACACTCAAACTGCAACACAAAACAACAAATTTATTGTCAGTGACAGTACCTACTCG 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIGGCAICCCCTTACTACAATA---CCTGCCCCTACTACTACTCCTCCT-----GCT 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 IlePheTyrThrPheSerThrValHisProlleProAspGluAspSerProTrplleThr 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTCACAGAAGTTTTTATG 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 AspSerThrAspArgileProAlaThrSer-----------Thr 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAG 863
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TGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATTAGCCCCAAACCCC 494
                          :::||| :::||| ::----ThrSer-----
                                                                                                                                                                 555 GCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT------
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---AsnProGluValLeuLeuGlnThrThrArgMetThrAspValAsp----
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Db 316ThrSerThrIleGlnAlaThrProSer	AlaThrGlnLyeGluGlnTrpPheGlyAsnArgTrpHisGluGlyTyrArg 347  AlaThrGlnLyeGluGlnTrpPheGlyAsnArgTrpHisGluGlyTyrArg 347  AgaaccaaggcTTTCTCTACTGATTCCGCAGCTCAGACCTTTCTTCAGCTCTGAAAGAG 159  ::	Qy         1596 AAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1643		SULT 15 02UG 090ZLG PRELIMINARY; 090ZLG;		4 11 12	RP SEQUENCE FROM N.A. RA Chan S.W.S., Middleton D.L., Lundqvist M., Warr G.W., Higgins D.A.; RT "Anas platyrhynchos T-cell antigens.";	KLD SUBMILLER (AFK-Z001) LO LHE EMBL/JUDSO WALADASES.  DR EMBL; AY032667; AAK52086.1;  DR GO; GO:0016020; C:membrane; IEA.  DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.	DR GO; GO:0005540; F:hyaluronic acid binding; IEA. DR GO; GO:0007155; P:cell adhesion; IEA. DR InterPor; IPR001231; C194_antigen. DR Trie-Pro; IPR000538: T.ink.	DR Pfam; PF00193; Xlink; 1. DR PRINTS; PR00659; CD44. DR PRINTS; PR01265; LINKMODULE. DR ProDom; PD000918; Link; 1.		Alignment Scores: 2.29e-11 Length: 168 Score: 206.50 Matches: 45 Percent Similarity: 52.34% Conservative: 22	: 35.16% Mismatches: 5.73% Indels: 13 Gaps:	US-10-079-111-2 (1-2029) x Q90ZL6 (1-168)  Qy 222 ATCTGGACGACGAGGCTCCTGGTCCAAGGCTCTTGCGAGAAGAGCTTTCCATCCA	9	Qy 282 GTGTCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAAT 341	342 TTCACAGAAGCTAAGAAGCCTGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAA 4
:::	CTCA 57	99 SeralaProProGluGluAspCysThrSerValThrAspLeuProAsnAlaPheAspGly 118 602	ArgThrasnProgluasp1leTyrProSerasnProThraspaspaspalSerSer3 15	654 CAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACA 713 :::::	714 ATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCA 764 :::	765 CGGAGAAAAAATTGATTTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACA 924 198 AlaThrSerThrSerSerAsnThrIleSerAla 208	825 GAAACTGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGA 884 209 GlyTrpGluProAsnGluGluAsnGluAspGluArgAspArgHisLeuSerPheSer 227	885 GGTGTCCCCACGGCTCTGCTAGTGCTTGCTCTCTTTTGGTGCTGCAGCTGGTCTT 944	945 GGAITITGCTAIGTCAAAAGGTAIGTGAAGGCCTTCCCTTTTACAAACAAACAAATCAGCAG 1004	AAGGAAATGATGGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAAT 10	1065 GAGGAATCAAAGAAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGGC 1115 	1116 AAAACTACCGTGCGATGCCTGGAAGCTGAAGTTTAGATGAGAACAGAAATGAGGACACA 1175	1176 CCTGAGGCTGGTTCTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAAATCAAAAGGGCC 1235	AAAGAACCAAAGAAAGTCCACCCTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCA	295ProglualaHisPro	315	1356 CTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTATGTCCTAATAATA 1415

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APPLICANT: Steve Daniel
APPLICANT: Steve Daniel
APPLICANT: Steve Daniel
APPLICANT: Suesn G. Stuart
APPLICANT: Laura Stuve
TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: PA-0003 US
CURRENT PAPLICATION NUMBER: US/09/232,160
CURRENT PALIENG DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PERL Program
SEQ ID NO 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 ATGGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCTGGACCACGAGGCTCCTG 242
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US-09-905-125A-213

US-09-902-775A-213

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US-09-902-775A-213

US-09-902-775A-3

US-09-206-695-5

US-09-799-118-5

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PCT-US95-04353-5
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US-08-478-322-6
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US-08-242-097-2
US-09-246-697-2
US-09-206-695-2
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US-08-225-477B-3
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US-08-225-477B-4
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Matches:
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US-09-232-160-21
 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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Sequence 201, App
Sequence 201, App
Sequence 201, Appl
Sequence 2, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 2, Appli
                                                                                                                        September 13, 2004, 10:13:27; Search time 36.5 Seconds (without alignments) 5739.676 Million cell updates/sec
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                                                                                                                                                                                                                                             Description
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                   - protein search, using frame_plus_n2p model
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US-09-907-794A-201
US-09-905-125A-201
US-09-902-775A-201
US-08-892-880-2
US-07-946-497-7
US-08-483-322-7
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                                                                                                                                                                                                                                                                                                                                                                                             389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                              Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Score 1657

Result

Jatabase :

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

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PRIOR FILING DATE: 1999-07-28

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PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-12-02

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PRIOR PILING DATE: 1999-12-03

PRIOR PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-12-03

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                                                                                                                                                                                                                                              Ь.
                                                                                                                                                                                                               Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                  Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.42e-174
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Filvaroff, Ellen
                                                                                                                                                Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Mather, Jennie P.
                                                                                                         Fong, Sherman
Gao, Wei-Qiang
                     Desnoyers, Luc
Saton, Dan L.
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3.09-07-794A-201
5.8equence 201, Application US/09907794A
Fatent No. 6635468
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
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Score:       1657.00       Matches:       322         Percent Similarity:       100.00\$       Conservative:       0         Best Local Similarity:       100.00\$       Mismatches:       0         Query Match:       4       45.98\$       Indels:       0         DB:       4       Gaps:       0         US-10-079-111-2 (1-2029)       x US-09-907-794A-201 (1-322)       0         Qy       183 ATGGCCAGGTGCTTCAGCTTCACTTCCACTTCCATTCCA	QY         243 GTCCAAGGCTCTTTGCGGCAGAAGAGCTTTCCATCCAGGGGTGTCATGCAGAATTATGGGG         302           Db         21 ValGlnGlySerLeuArgAlaGluGluLeuSerlleGlnValSerCysArgIleMetGly         40           QY         303 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGGAGGCC         362           Db         41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla         60	363 61 423 81	Qy         483 AGCCCAAACCCCAAGTGTGGGAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG 542           Db         101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120           Qy         543 AGCCGACAGTTTGCAGCCTATTGTACAACTCATCTGAACTTGGACTAACTCGTGCATT         602           Db         121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140	QY         603 CCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACAACAAACA	QY         723 CCTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGGAAAAAATTGATT 782           Db         181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle 200           QY         783 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 842           Db         201 CysValThrGluValPheMetGluThrSerThrMetSerThrMetSerThrGluPhrGluPhrGluPhroPheVal 220	843 GAAATAAAGCAGCATTCAAGAATGAAGCTGGGGTTTGGAGGTGTCCCCACGGCTCTG [	Qy         963 AGGTATCTGAAGGCTTTTACAAACAGGAATCGTGGAACC           Db         261 AGGTATCTGAAGCCTTTTACAAACAGGAATCGTGGAACC           Db         261 AGGTATCTGAAGGAGACAACAGATGATGAAAGAAACTIGGIUThr           Qy         1023 AAAGTAGTAAAGGAGGAGAAGGCCAATGATGATAGCAACCCTAATGAAGGAAACT         1082           Db         281 LysValValLysGluGluLysAlaAsnABSEAANPrOASGIUGLUSETLYSLYSThr         300           Qy         1083 GATAAAAACCCAGAAGGTCCAAGAGTCCAAGCAAAACTGCTGGGAGGTTI42         Db           Db         301 AspLysAsnProGluGluSerLysErProSerLysThrThrValArgCysLeuGluAla         320           Qy         1143 GAAGTT 1148

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APPLICANT: Tumas, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT APPLICATION NUMBER: US/00/0414
PRIOR APPLICATION NUMBER: US/01/45,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-15
PRIOR PLICATION NUMBER: PCT/US99/2054
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
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1 Sequence 201, Application US/09902775A

2 Sequence 201, Application US/09902775A

3 PATCHT NO. 668651

4 APPLICANT: Geneatech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David
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Goddard, A.
Goddwski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, James
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
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Eaton, Dan L.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                         US-10-079-111-2 (1-2029) x US-09-905-125A-201 (1-322)
                                                                                                                                                                                                                                                                       Gaps:
                                                                           FEATURE: OTHER INFORMATION: Synthetic protein
                                                                                                                                                                         5.42e-174
1657.00
100.00%
100.00%
45.98%
                                     TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                     ; OTHER INFORMAT:
US-09-905-125A-201
                                                                                                                                                       ignment Scores:
1Q ID NO 201
LENGTH: 322
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      AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC
                                                                                                                                        261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr
                                                                                                                                                                                                     281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGerLysLysThr
                                                                                                                                                                                                                                                                 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla
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                                                      CTAGTGCTTGCTCCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA
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CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGRNT INFORMATION:
NAME: STEFFE, RRIC K
REGISTRATION NUMBER: 35,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.L.L.
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 5942417

GENERAL INFORMATION:

APPLICANT: GENTZ, REINER L.

APPLICANT: GILLON, PARRICK J.

TITLE OF INVENTION: CD44-LIKE PROTEIN

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: 3100 NEW YORK AVENUE, NW, SUITE 600

CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0490001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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1651.00
99.69%
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amino acid
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Best Local Similarity:
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SQU ID NO 201
LENGTH: 322
                                                                                                                                                                                                                           FEATURE:
; OTHER INFORMATION: Synthetic protein US-09-902-775A-201
                                                                                                                                                                                                                                                                                                           5.42e-174
1657.00
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ORGANISM: Artificial sequence
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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LENGTH: 318
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                                         ATGGCCAGGTGCTTCAGCCTGCTGTTCTCACTTCCATCTGGACCACGAGGCTCCTG
                                                                                                                                      CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla
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                                                     21 ValGlnGlySerLeuArgAlaGluGluLeuSerlleGlnValSerCysArg1leMetGly
                                                                                                                           ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC
                                                                                                                                                                   TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT
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                  US-10-079-111-2 (1-2029) x US-08-892-880-2 (1-322)
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Sequence 60, Application US/09724864
Fatent No. 6380362
GENERAL INFORMATION:
APPLICANT: Watson, James D
TITLE OF INVENTION: POLYMUCLEOTIDES, polypeptides expressed
TITLE OF INVENTION: Dy the polymucleotides and methods for their use.
FILE REFERENCE: 11000.105001
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
FILMS DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FRSESEQ for Windows Version 4.0
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221
30
62
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Matches:
Conservative:
Mismatches:
Indels:
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79.18%
69.72%
30.60%
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Best Local Similarity:
Query Match:
DB:
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Query Match:         6.42*         Indels:         63           DB:         1         14         14           US-10-079-111-2 (1-2029) x US-07-946-497-7 (1-363)         0         225 TGGACCACGAGGCTCCTGGTCCAAGGCTTTTGCTGAGAAGAGTTTCC 275           QY         225 TGGACCACGAGG	396 456 656 85 105 105	Qy         636 AACACTCAAACTGCAACACAACAACAATTTATTGTCAGTGACAGTACCTACTCG 692           III	### ### ##############################	CY 1035 GAGGAGGCAATGGCAACCCTAATGGGGAATCAAAGAAAATGAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAA
Db   202 TyrThrGluProlleThrMetAlaThrGluAlaPheValAlaSerGlyAlaAla 221   858 TTCAAGAATGAAGCTGCTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTCC 917   1   1   1   1   1   1   1   1   1	STECAGGAAACTACGGTGGGATGCCTGGAAGCTGAAGT 1148  STEPOPTOLYSTATTATVALATGCYSLEUGIUALAGIUVAL 318  1 US/07946497  1, Peter lelmut  1, Usula  1,	NAME OF STREET	45 enorth.	imilarity: 24.93%

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984 TTTACAAACAAGAATCAGCAGAAGGAAATGATC-----GAAACCAAAGTAGTAAAG 1034
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314 AsparglysProSerGluLeuAsn---GlyGluAlaSerLysSerGlnGluMetValHis 332
                                         GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGA 455
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105 ||'yValTyrIleLeuValThrSerAsnThrSerHisTyrAspThrTyrCysPheAsnAla 124
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46 IleSerArqThrGluAlaAlaAspLeuCysGlnAlaPheAsnSerThrLeuProThrMet 65
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                                                                     GATGGATTCGTGGTCATCTCTAGGATTAGCCCCAAACCCCCAAGTGTGGGGAAAAATGGGGGTG
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Patent No. 5885575
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APPLICANT: HERRLICH, Peter
APPLICANT: PONTA, Helmut
APPLICANT: GUENTHERT, Ursula
APPLICANT: MATZKU, Siegfried
APPLICANT: WENZKU, Achim
IITLE OF INVENTION: VARIANT CDA
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                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: HERRLICH, Peter

APPLICANT: FONTA, Helmut

APPLICANT: GURNTHERT, Useula

APPLICANT: MATZKU, Siegfried

APPLICANT: WENZL, Achim

TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,

TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
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    1095 GAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCTGAA 1145
                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,322
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: A35
PRIOR APPLICATION NUMBER: US 07/946,497
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
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Conservative:
Mismatches:
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                                                                                                                       Sequence 7, Application US/08483322
Patent No. 5760178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 165 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W. CIIY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
TELEX: 9
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Query Match:
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TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1035 GAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACTGATAAAAACCCA 1094
                                                                                                 140 AsnSerPheAspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSer 159
                                                                                                                                         728
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            ---ThrSerValThrAspLeuPro 139
                                                                                                                                                                          LysLysGlyGluTyrArgThrHisGlnGluAspileAspAlaSerAsnIleIleAspAsp 179
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                                                                                                                                                                                                                                           240 HisGlySerGluLeuAlaGlyHisSerSerAlaAsnGlnAspSerGlyValThrThr
                                                                                                                                                                                                                --ACTACTCCTCCTGCT---CCAGCTTCCACT
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                                                                                                                                                                                                                                                                                                                                  TyrLeuProThrGluGlnProThrGlyAspGlnAspAspSerPhePheIleArgSerThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 LeuValAsnLysGluProSerGluThrProAspGlnCysMetThrAlaAsp 349
                                                                                                                                                                                                                                                                                                                                                                           816 AIGTCTACA---GAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAG-
                                                                                                                                         --ATACCTGCCCCTACT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 LeuAlaLeuAlaLeuIleLeuAlaValCys---
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                      SerAlaProProGluGluAspCys----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/07946497
Patent No. 5506119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PONTA, Helmut
GUENTHERT, Ursula
MATZKU, Siegfried
WENZL, Achim
                                                                                                                                     693 GIGGCATCCCCTTACTCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HERRLICH, Peter
APPLICANT: PONTA, Helmut
APPLICANT: GUENTHERT, Uraul
APPLICANT: MATZKU, Siegfrie
APPLICANT: WENZL, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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GENERAL IN
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  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 ATCCAGGTGTCATGCCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGCAG 335
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| GlyValTyrIleLeuValThrSerAsnThrSerHisTyrAspThrTyrCysPheAsnAla 124
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89
148
63
                                                                                                                                              ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,882
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                           SEE: Foley & Lardner
: 3000 K Street, N.W., Suite 500
Washington, D.C.
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946,497
FILING DATE: 19921109
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904135
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
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231.50
40.90%
24.93%
6.42%
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TELEPHONE: (202)c.
TELEPHONE: (202) 672-5399
TITLE OF INVENTION: SE
TITLE OF INVENTION: AS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: mCD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                     USA
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                                                                           ADDRESSEE:
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                                                                                                                                 COUNTRY:
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VARIANT CD44 SURFACE PROTEINS, DNA
SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
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                                                                                                                                                                                                                                                                     284 AsnAsnHisGluTyrdlnAspGluGluGluGluThrProHisAlaThrSerThrThrTrpAla 303
                                                                                                                                                                                                                                                                                                                                                304 AspProAsnSerThrThrGluGluAlaAlaThrGlnLysGluLysTrpPheGluAsnGlu 323
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       ---GAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTT 881
                               .017 GAAACCAAAGTAGTAAAGGAGAGAGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAG
                                                                                                                                                                                                                                                                                                                                                                                     1077 AAAACTGATAAAAACCCA-----GAAGAGTCCAAGAGTCCAAGGATCCAAACTACC
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411 TrpLeu--IleIleLeuAlaSerLeuLeuAlaLeuAlaLeuIleLeuAlaValCys----
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                                                                                                                     244 AsnProlleHisSerAsnProGluValLeuLeuGlnThrThrThrArgMetThrAsplle
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US-08-483-322-2
; Sequence 2, Application US/08483322
; Patent No. 5760178
; GENERAL INFORMATION:
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APPLICANT: PONTA, Helmut
APPLICANT: GUENTHERT, Ursula
APPLICANT: MATZKU, Siegfried
APPLICANT: WENZL, Achim
TITLE OF INVENTION: VARIANT CD4
TITLE OF INVENTION: SEQUENCES CTITLE OF INVENTION: AS WELL AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               645 ACTGCAACACAACAACAACTTTATTGTCAGTGACAGTACC---TACTCGGTGGCATCC 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 GluTyrArgThrHisGlnGluAspileAspAlaSerAsnIleIleAspGluAspValSer 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 TCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTC
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50 ThrGluhlaAlaAspLeuCysGluAlaPheAsnThrThrLeuProThrMetAlaGlnMet
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Matches:
Conservative:
Mismatches:
Indele:
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APPLICATION NUMBER: US/07/946,497
CLASSIPICATION: 435
ATTORNEY/AGENT INPERMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                             4.64e-16
228.50
36.19%
24.51%
6.34%
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                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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.017 GAAACCAAAGTAGTAAAGGAGGAGAAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAG 1076
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                                                                                                                GluTyrArgThrHisGlnGluAspileAspAlaSerAsnIleIleAspGluAspValSer 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 AlaSerAlaHisAsnAsnHisProSerGlnArgMetThrThrGlnSerGlnGluAspVal 363
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364 SerTrpThrAspPhePheAsp---ProlleSerHisProMetGlyGln------Gly 379
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445 IleAsnSerGlyAsnGlyThrValGluAspArgLysProSerGluLeuAsnGlyGluAla 464
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                                                                                                                                                                       144 AspGlyProValThr1leThr1leValAsnArgAspGlyThrArgTyrSerLysLysGly
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ThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSerIleSerArg
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                                                                                                   ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDTION TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATCHILIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,322
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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Mismatches:
Indels:
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Matches:
                                    SEE: Foley & Lardner: 3000 K Street, N.W., Suite 500 Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,497
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELERAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 503 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.64e-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 503 amino acids
amino acid
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36.19%
24.51%
6.34%
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                  CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                    CITY: Wa
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-ATGATC 1016

-- AAGGCC 1490

1548 ITCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA 1583

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1350 IGGAICCIAICCICCIACCICCAAAGCIICCCACGGCCIIICIAGCCIGGCIAIGICCIA 1409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 AsnAshHisGluTyrdlnAspGluGluGluThrProHisAlaThrSerThrThrTrpAla 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTT 881
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                                                                                                                                                                                         89 ValValileProArgileHisProAsnAlaIleCysAlaAlaAsnAsnThrGlyValTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SerSerGly---Asn
GAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGCATTC
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                                                                                                                                                                                                                                                             525 ATTIGGAAGGITCCAGIGAGCCGACAGITIGCAGCCIAITGITACAACTCAICTGAIACI
                                                                                                                                                                                                                                                                                                                                                                                             585 TGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          933 GCAGCTGGTCTTGGATTTTGCTATGTCAAAGGTATGTGAAG------GCCTTCCCTTTT
                                                                                                                                   ---ACTACTCCTCCTGCT----CCAGCTTCCACTTCTATTCCA
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                                                                                                                                                 Sequence 2, Application US/08478882
Sequence 2, Application US/08478882
Sequence 2, Application US/08478882
Series No. 5885575
GENERAL INFORMATION:
APPLICANT: HERRILCH, Peter
APPLICANT: GUENTHERT, Ursula
APPLICANT: GUENTHERT, Ursula
APPLICANT: MINAZU, Segfirled
APPLICANT: SEQUENCES CODING THESE, ANTHRODIES AGAINST THESE PROTEINS, TITLE OF INVENTION: SEQUENCES: 8
CORRESPONDENCE ADDRESS: 8
CORRESPONDENCE ADDRESS: SEQUENCES: 8
CORRESPONDENCE ADDRESS: SECUENCES: SEQUENCES:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTC 344
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TrpGlyLeuLeuCysLeuLeuGlnLeuSerLeuAlaGlnGlnGlnIleAspLeuAsnIle 29
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ThrCygArgTyrAlaGlyValPheHisValGluLygAnGlyArgTyrSerIleSerArg 49
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ThrGluAlaAlaAspLeuCysGluAlaPheAsnThrThrLeuProThrMetAlaGlnMet 69
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126
60
242
86
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,882
FILING DATE:
                Length:
Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946,497
FILING DATE: 19921109
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
TELECOMMUNICATION:
TELEPHONE: (202)672-5309
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: 3000 K Street, N.W., Suite
Washington, D.C.
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
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CITY: Wa
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50 ThrGluAlaAspLeuCysGluAlaPheAsnThrThrLeuProThrMetAlaGlmMet 69
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                                              |||| TrpdlyLeuLeuCysLeuLeuGlnLeuSerLeuAlaGlnGlnGlnIleAspLeuAsnIle
                                                                                                         GIGGICALCICIAGGAITAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTG
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                                                                       ------IleAlaValAsnSerArgArgArgCysGlyGlnLysLysLysLuVal-
                                                                                                                                                              1491 TCCTGGCTGTCTGAGGCTAGGTGGGGTTGAAAGCCAAGGAGTCACTGAGACC---AAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTRY: USA
ZIP: 20005-3934
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRR: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HERBWITH
APSTORMED ATS: TOS/08/892,880
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Matches:
Conservative:
Mismatches:
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APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
ITILE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08892880 Patent No. 5942417 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                     1470 GTATCCAGTGGTAAA---
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MOLECULE TYPE: protein

US-08-892-880-3
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Query Match:
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-------ThrSerValThrAspLeuProAsnAlaPheAspGlyProIleThr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 IleThrIleValAsnArgAspGlyThrArgTyrValLysLysGlyGluTyrArgThrAsn 164
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| 185 GluargSerSerThrLeuGlyGlyTyrIlePheTyrAsnHisPheSerThrSerProPro
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        TITLE OF INVENTION: LYMPHOCYTE ADHESION RECEPTOR FOR HIGH
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                        (1-362)
                                NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/884,624
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 628,646
FILING DATE: 12-DEC-1990
APPLICATION NUMBER: 325,224
FILING DATE: 17-MAR-1989
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APPLICANT: HERRLICH, Peter
APPLICANT: PONTA, Helmut
APPLICANT: PONTA, Helmut
APPLICANT: GUENTHERT, Ursula
APPLICANT: MAZKU, Siegfried
APPLICANT: WRIZL, Achim
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
CORRESPONDENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLLY & LAIGHGE
                                                                                                                                                                                                                                                                                                                                                                                                              1068 GAATCAAAGAAAACTGATAAA------AACCCAGAAGAGTCCAAGAGTCCAAGC 1115
                                                                                                                                                                                                                                           957 GICAAAAGGIAIGIGAAGGCCTICCCITITACAAACAAGAATCAGCAGAAGGAAAIGAIC 1016
                                                                                                                                                                                                                                                                                                                               -GTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAG 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                           304 IleAsnAsnGlyAsnGlyAlaValGluAspArgLySserSerGlyLeuAsn---GlyGlu 322
                                                                                                              250 SerArgGluĠlyĠlyAlaAsnThrThrSerGlyProLeuArgThrProGlnIleProGlu 269
                                                                                                                                                                                    897 GCTCTGCTAGTGCTTGCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTAT
                 PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Foley & Lardner
: 3000 K Street, N.W., Suite 500
Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Palana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/946,497
FILING DATE: 19921109
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/07946497
Patent No. 5506119
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
ELNGTH: 361 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (202) 672-5399
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                                                                                                                                                                                                                                                                                                                                        1017 GAAACCAAA-----
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861 AAG-
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CITY: Wa
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US-07-946-497-6

Alignment Pred. No.: Score: Percent Si Best Local Query Matc	t Scores: .: Similarity: al Similarity: tch:	9.1e-14 307.00 38.24% 24.41% 5.74%	Length: Matches: Conservative: Mismatches: Indels:	361 83 147 66 14
US-10-07	9-111-2 (1-2029	9) x US-07-946-4	497-6 (1-361)	
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ì ò	5 AGCAA	ALEGITTERSPIEC 3GCGAACCAGCTG	ASHITCACAGAAGCT	AAGGAAGCCTGTAAGGCTGCTG 374
7 A	37 GluLy	 sAsnGlyArgTyrSerIle	erIleSerArgThrGluAla	, 9
ò	375 GGACTAAGI	rttggccggcaagaac	CTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTT	TIGAAAGCTAGCTITIGAAACT 434
ΩÞ	57 AsnSerThrL	:     rLeuProThrMetAla	:::     aGlnMetGluLysAla	 uSerIleGlyPheGluT
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d	115 AspThrTyr	.CysPheAsnAlaSer	erAlaProProGluGluAspCys	AspCys 129
ò	₫	CCAAAGATCCCATATTCAACACT	ACTCAAACTGCAACACAAA	CAAACAACAGAATTTATTGTC 674
qq	Н	euProA	snAlaPheAspGlyProIl	eThrileThrileVa
δλ	675 AGTGACAGTA	PACCTACTCGGTGGCAT	GCATCCCCTTACTCTA	ACAATACCTGCC 722
DÞ	150 ArgAspGly	ThrArgTyrValGln	yThrargTyrValGlnLysGlyGluTyrArgThra	ThrAsnProGluAspIleTyr 169
λŏ	[[	ACTCCTCCTGCTCCA	AGCTTCCACTTCTATT	ACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT 782
qq	erA	snProThrAspAspAsp	spValSerSerGlySer	SerSerGluArgSerSerThr 189
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ò	819	Ē	ACTGAACCATTIGIT	CTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTC 860
qq	210 ProTrpile	eThrAspSerThrAsp	ArgileProAl	aThrArgAspGlnAspThrPheHis 229
ò	861		GAATGAAG	GCTGGGTTT 881
qa	230 ProSerGlyGl	'GlySerHisThrThrHi	:::   ::: :HisGluSerGluSerA	   AspGlyHisSerHisGlySer 249
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ζ	900 CTGCTAGTG	CTAGTGCTTGCTCTCCTCTTC	CTTTGGTGCTGCAGCT	CTGGTCTTGGATTTTGCTATGTC 959
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qa	287	::: :IleAlaValAsnSerArgAr	gArgCysGl	:::   :::   yGlnLysLysLysLeuValIle 303
<b>%</b>	1020 ACCAAA	GTAGTAAAG	GAGGAGAAGGCCAAT	GTAGTAAAGGAGGAGAAAGCCCAATGATAGCAACCCTAATGAGGAA 1070

	1071 TCAAGGAAACTGATAAAAACCCAGAAGAGGTCCAAGGAAA 1118	
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Search completed: September 13, 2004, 10:33:31 Job time : 53.5 secs

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